

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

(A) NAME: BRIGHAM AND WOMEN'S HOSPITAL
(B) STREET: 75 FRANCIS STREET
(C) CITY: BOSTON
(D) STATE: MASSACHUSETTS
(E) COUNTRY: USA
(F) POSTAL CODE (ZIP): 02115
(A) NAME: DANA-FARBER CANCER INSTITUTE
(B) STREET: 44 BINNEY STREET
(C) CITY: BOSTON
(D) STATE: MASSACHUSETTS
(E) COUNTRY: USA
(F) POSTAL CODE (ZIP): 02115

(ii) TITLE OF INVENTION: Novel Forms of T Cell Costimulatory Molecules
and Uses Therefor

(iii) NUMBER OF SEQUENCES: 65

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: LAHIVE & COCKFIELD
(B) STREET: 60 State Street, suite 510
(C) CITY: Boston
(D) STATE: Massachusetts
(E) COUNTRY: USA
(F) ZIP: 02109-1875

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: ASCII Text

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/205,697
(B) FILING DATE: 02-Mar-1994

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Mandragouras, Amy E.
(B) REGISTRATION NUMBER: 36,207
(C) REFERENCE/DOCKET NUMBER: BWI-120CPPC

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (617) 227-7400
(B) TELEFAX: (617) 227-5941

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1888 base pairs

960220 52520780

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

10 (A) NAME/KEY: CDS
 (B) LOCATION: 249..1208

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

15 GAGTTTATA CCTCAATAGA CTCTTACTAG TTTCTCTTTT TCAGGTTGTG AAACCTCAACC 60
 TTCAAAGACA CTCTGTTCCA TTTCTGTGGA CTAATAGGAT CATCTTTAGC ATCTGCCGGG 120
 20 TGGATGCCAT CCAGGCTTCT TTTTCTACAT CTCTGTTTCT CGATTTTGTG GAGCCTAGGA 180
 GGTGCCTAAG CTCCATTGGC TCTAGATTCC TGGCTTTCCC CATCATGTTT TCCAAAGCAT 240
 CTGAAGCT ATG GCT TGC AAT TGT CAG TTG ATG CAG GAT ACA CCA CTC CTC 290
 Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu
 25 1 5 10
 AAG TTT CCA TGT CCA AGG CTC AAT CTT CTC TTT GTG CTG CTG ATT CGT 338
 Lys Phe Pro Cys Pro Arg Leu Asn Leu Leu Phe Val Leu Leu Ile Arg
 15 20 25 30
 CTT TCA CAA GTG TCT TCA GAT GTT GAT GAA CAA CTG TCC AAG TCA GTG 386
 Leu Ser Gln Val Ser Ser Asp Val Asp Glu Gln Leu Ser Lys Ser Val
 35 35 40 45
 AAA GAT AAG GTA TTG CTG CCT TGC CGT TAC AAC TCT CCT CAT GAA GAT 434
 Lys Asp Lys Val Leu Leu Pro Cys Arg Tyr Asn Ser Pro His Glu Asp
 50 55 60
 GAG TCT GAA GAC CGA ATC TAC TGG CAA AAA CAT GAC AAA GTG GTG CTG 482
 Glu Ser Glu Asp Arg Ile Tyr Trp Gln Lys His Asp Lys Val Val Leu
 65 70 75
 TCT GTC ATT GCT GGG AAA CTA AAA GTG TGG CCC GAG TAT AAG AAC CGG 530
 Ser Val Ile Ala Gly Lys Leu Lys Val Trp Pro Glu Tyr Lys Asn Arg
 45 80 85 90
 ACT TTA TAT GAC AAC ACT ACC TAC TCT CTT ATC ATC CTG GGC CTG GTC 578
 Thr Leu Tyr Asp Asn Thr Thr Tyr Ser Leu Ile Ile Leu Gly Leu Val
 95 100 105 110
 CTT TCA GAC CGG GGC ACA TAC AGC TGT GTC GTT CAA AAG AAG GAA AGA 626
 Leu Ser Asp Arg Gly Thr Tyr Ser Cys Val Val Gln Lys Lys Glu Arg
 115 120 125
 55 GGA ACG TAT GAA GTT AAA CAC TTG GCT TTA GTA AAG TTG TCC ATC AAA 674
 Gly Thr Tyr Glu Val Lys His Leu Ala Leu Val Lys Leu Ser Ile Lys
 130 135 140

08702525 52520280

	GCT GAC TTC TCT ACC CCC AAC ATA ACT GAG TCT GGA AAC CCA TCT GCA	722
	Ala Asp Phe Ser Thr Pro Asn Ile Thr Glu Ser Gly Asn Pro Ser Ala	
	145 150 155	
5	GAC ACT AAA AGG ATT ACC TGC TTT GCT TCC GGG GGT TTC CCA AAG CCT	770
	Asp Thr Lys Arg Ile Thr Cys Phe Ala Ser Gly Gly Phe Pro Lys Pro	
	160 165 170	
10	CGC TTC TCT TGG TTG GAA AAT GGA AGA GAA TTA CCT GGC ATC AAT ACG	818
	Arg Phe Ser Trp Leu Glu Asn Gly Arg Glu Leu Pro Gly Ile Asn Thr	
	175 180 185 190	
15	ACA ATT TCC CAG GAT CCT GAA TCT GAA TTG TAC ACC ATT AGT AGC CAA	866
	Thr Ile Ser Gln Asp Pro Glu Ser Glu Leu Tyr Thr Ile Ser Ser Gln	
	195 200 205	
	CTA GAT TTC AAT ACG ACT CGC AAC CAC ACC ATT AAG TGT CTC ATT AAA	914
	Leu Asp Phe Asn Thr Thr Arg Asn His Thr Ile Lys Cys Leu Ile Lys	
	210 215 220	
20	TAT GGA GAT GCT CAC GTG TCA GAG GAC TTC ACC TGG GAA AAA CCC CCA	962
	Tyr Gly Asp Ala His Val Ser Glu Asp Phe Thr Trp Glu Lys Pro Pro	
	225 230 235	
25	GAA GAC CCT CCT GAT AGC AAG AAC ACA CTT GTG CTC TTT GGG GCA GGA	1010
	Glu Asp Pro Pro Asp Ser Lys Asn Thr Leu Val Leu Phe Gly Ala Gly	
	240 245 250	
30	TTC GGC GCA GTA ATA ACA GTC GTC GTC ATC GTT GTC ATC ATC AAA TGC	1058
	Phe Gly Ala Val Ile Thr Val Val Val Ile Val Val Ile Ile Lys Cys	
	255 260 265 270	
35	TTC TGT AAG CAC GGT CTC ATC TAC CAT TTG CAA CTG ACC TCT TCT GCA	1106
	Phe Cys Lys His Gly Leu Ile Tyr His Leu Gln Leu Thr Ser Ser Ala	
	275 280 285	
	AAG GAC TTC AGA AAC CTA GCA CTA CCC TGG CTC TGC AAA CAC GGT TCT	1154
	Lys Asp Phe Arg Asn Leu Ala Leu Pro Trp Leu Cys Lys His Gly Ser	
	290 295 300	
40	CTA GGT GAA GCC TCT GCA GTG ATT TGC AGA AGT ACT CAG ACG AAT GAA	1202
	Leu Gly Glu Ala Ser Ala Val Ile Cys Arg Ser Thr Gln Thr Asn Glu	
	305 310 315	
45	CCA CAG TAGTTCTGCT GTTTCTGAGG ACGTAGTTTA GAGACTGAAT TCTTTGAAA	1258
	Pro Gln	
	320	
50	GGACATAGGG ACAGTTTGCA CATTTGCTTG CACATCACAC ACACACACAC ACACACACAC	1318
	ACACACACAC ACACACACAC ACACACACAC ACACACACAC TCTCTCTCTC TCTCTCTCTC	1378
	GATACCTTAG GATAGGGTTC TACCCTGTTG CTCAGTGACA AAGAATCACT CTGTGGCGGA	1438
55	GGCAGGCTTC AAGCTTGCAG CAATCCTCCT GCACCAGTTT CCTGAGTGCC AGACTTCCAG	1498
	GTGTAAGCTA TGGCACTTAG CAGAACAATA GCTGAATCAA TGAAGACACT GAGGTTCCAA	1558
	GAGGGAACCT GAATTATGAA GGTGAGTCAG AATCCAGATT TCCTGGCTCT ACCACTCTTA	1618

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5 ACCTGTATCT GTTAGACCCC AAGCTCTGAG CTCATAGACA AGCTAATTTA AAATGCTTTT 1678
 TAATAAGCAG AAGGCTCAGT TAGTACGGGG TTCAGGATAC TGCTTACTGG CAATATTTGA 1738
 CTAGCCTCTA TTTTGTGTTGT TTTTAAAGG CCTACTGACT GTAGTGTAAAT TTGTAGGAAA 1798
 CATGTTGCTA TGTATACCCA TTTGAGGGTA ATAAAAATGT TGGTAATTTT CAGCCAGCAC 1858
 10 TTTCCAGGTA TTTCCCTTTT TATCCTTCAT 1888

(2) INFORMATION FOR SEQ ID NO:2:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 320 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

25 Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu Lys Phe
 1 5 10 15
 Pro Cys Pro Arg Leu Asn Leu Leu Phe Val Leu Leu Ile Arg Leu Ser
 20 25 30
 30 Gln Val Ser Ser Asp Val Asp Glu Gln Leu Ser Lys Ser Val Lys Asp
 35 40 45
 Lys Val Leu Leu Pro Cys Arg Tyr Asn Ser Pro His Glu Asp Glu Ser
 50 55 60
 35 Glu Asp Arg Ile Tyr Trp Gln Lys His Asp Lys Val Val Leu Ser Val
 65 70 75 80
 40 Ile Ala Gly Lys Leu Lys Val Trp Pro Glu Tyr Lys Asn Arg Thr Leu
 85 90 95
 Tyr Asp Asn Thr Thr Tyr Ser Leu Ile Ile Leu Gly Leu Val Leu Ser
 100 105 110
 45 Asp Arg Gly Thr Tyr Ser Cys Val Val Gln Lys Lys Glu Arg Gly Thr
 115 120 125
 Tyr Glu Val Lys His Leu Ala Leu Val Lys Leu Ser Ile Lys Ala Asp
 130 135 140
 50 Phe Ser Thr Pro Asn Ile Thr Glu Ser Gly Asn Pro Ser Ala Asp Thr
 145 150 155 160
 55 Lys Arg Ile Thr Cys Phe Ala Ser Gly Gly Phe Pro Lys Pro Arg Phe
 165 170 175
 Ser Trp Leu Glu Asn Gly Arg Glu Leu Pro Gly Ile Asn Thr Thr Ile
 180 185 190

0870255-083095
 960E80-58520280

Ser Gln Asp Pro Glu Ser Glu Leu Tyr Thr Ile Ser Ser Gln Leu Asp
195 200 205

Phe Asn Thr Thr Arg Asn His Thr Ile Lys Cys Leu Ile Lys Tyr Gly
210 215 220

Asp Ala His Val Ser Glu Asp Phe Thr Trp Glu Lys Pro Pro Glu Asp
225 230 235 240

Pro Pro Asp Ser Lys Asn Thr Leu Val Leu Phe Gly Ala Gly Phe Gly
245 250 255

Ala Val Ile Thr Val Val Val Ile Val Val Ile Ile Lys Cys Phe Cys
260 265 270

Lys His Gly Leu Ile Tyr His Leu Gln Leu Thr Ser Ser Ala Lys Asp
275 280 285

Phe Arg Asn Leu Ala Leu Pro Trp Leu Cys Lys His Gly Ser Leu Gly
290 295 300

Glu Ala Ser Ala Val Ile Cys Arg Ser Thr Gln Thr Asn Glu Pro Gln
305 310 315 320

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2516 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 249..1166

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAGTTTATA CCTCAATAGA CTCTTACTAG TTTCTCTTTT TCAGGTTGTG AAACCTCAACC 60
TTCAAAGACA CTCTGTTCCA TTTCTGTGGA CTAATAGGAT CATCTTTAGC ATCTGCCGGG 120
TGGATGCCAT CCAGGCTTCT TTTTCTACAT CTCTGTTTCT CGATTTTGTG GAGCCTAGGA 180
GGTGCCTAAG CTCCATTGGC TCTAGATTCC TGGCTTTCCC CATCATGTTC TCCAAAGCAT 240
CTGAAGCT ATG GCT TGC AAT TGT CAG TTG ATG CAG GAT ACA CCA CTC CTC 290
Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu
1 5 10
AAG TTT CCA TGT CCA AGG CTC AAT CTT CTC TTT GTG CTG CTG AAT CGT 338
Lys Phe Pro Cys Pro Arg Leu Asn Leu Leu Phe Val Leu Leu Asn Arg
15 20 25 30

08702555 0083096
960E80 52520/80

	CTT TCA CAA GTG TCT TCA GAT GTT GAT GAA CAA CTG TCC AAG TCA GTG Leu Ser Gln Val Ser Ser Asp Val Asp Glu Gln Leu Ser Lys Ser Val	386
	35 40 45	
5	AAA GAT AAG GTA TTG CTG CCT TGC CGT TAC AAC TCT CCT CAT GAA GAT Lys Asp Lys Val Leu Leu Pro Cys Arg Tyr Asn Ser Pro His Glu Asp	434
	50 55 60	
10	GAG TCT GAA GAC CGA ATC TAC TGG GAA AAA CAT GAC AAA GTG GTG CTG Glu Ser Glu Asp Arg Ile Tyr Trp Gln Lys His Asp Lys Val Val Leu	482
	65 70 75	
15	TCT GTC ATT GCT GGG AAA CTA AAA GTG TGG CCC GAG TAT AAG AAC CGG Ser Val Ile Ala Gly Lys Leu Lys Val Trp Pro Glu Tyr Lys Asn Arg	530
	80 85 90	
20	ACT TTA TAT GAC AAC ACT ACC TAC TCT CTT ATC ATC CTG GGC CTG GTC Thr Leu Tyr Asp Asn Thr Thr Tyr Ser Leu Ile Ile Leu Gly Leu Val	578
	95 100 105 110	
25	CTT TCA GAC CGG GGC ACA TAC AGC TGT GTC GTT CAA AAG AAG GAA AGA Leu Ser Asp Arg Gly Thr Tyr Ser Cys Val Val Gln Lys Lys Glu Arg	626
	115 120 125	
30	GGA ACG TAT GAA GTT AAA CAC TTG GCT TTA GTA AAG TTG TCC ATC AAA Gly Thr Tyr Glu Val Lys His Leu Ala Leu Val Lys Leu Ser Ile Lys	674
	130 135 140	
35	GCT GAC TTC TCT ACC CCC AAC ATA ACT GAG TCT GGA AAC CCA TCT GCA Ala Asp Phe Ser Thr Pro Asn Ile Thr Glu Ser Gly Asn Pro Ser Ala	722
	145 150 155	
40	GAC ACT AAA AGG ATT ACC TGC TTT GCT TCC GGG GGT TTC CCA AAG CCT Asp Thr Lys Arg Ile Thr Cys Phe Ala Ser Gly Glu Phe Pro Lys Pro	770
	160 165 170	
45	CGC TTC TCT TGG TTG GAA AAT GGA AGA GAA TTA CCT GGC ATC AAT ACG Arg Phe Ser Trp Leu Glu Asn Gly Arg Glu Leu Pro Gly Ile Asn Thr	818
	175 180 185 190	
50	ACA ATT TCC CAG GAT CCT GAA TCT GAA TTG TAC ACC ATT AGT AGC CAA Thr Ile Ser Gln Asp Pro Glu Ser Glu Leu Tyr Thr Ile Ser Ser Gln	866
	195 200 205	
55	CTA GAT TTC AAT ACG ACT CGC AAC CAC ACC ATT AAG TGT CTC ATT AAA Leu Asp Phe Asn Thr Thr Arg Asn His Thr Ile Lys Cys Leu Ile Lys	914
	210 215 220	
60	TAT GGA GAT GCT CAC GTG TCA GAG GAC TTC ACC TGG GAA AAA CCC CCA Tyr Gly Asp Ala His Val Ser Glu Asp Phe Thr Trp Glu Lys Pro Pro	962
	225 230 235	
65	GAA GAC CCT CCT GAT AGC AAG AAC ACA CTT GTG CTC TTT GGG GCA GGA Glu Asp Pro Pro Asp Ser Lys Asn Thr Leu Val Phe Gly Ala Gly	1010
	240 245 250	
70	TTC GGC GCA GTA ATA ACA GTC GTC GTC ATC GTT GTC ATC ATC AAA TGC Phe Gly Ala Val Ile Thr Val Val Val Ile Val Val Ile Ile Lys Cys	1058
	255 260 265 270	

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5 TTC TGT AAG CAC AGA AGC TGT TTC AGA AGA AAT GAG GCA AGC AGA GAA 1106
Phe Cys Lys His Arg Ser Cys Phe Arg Arg Asn Glu Ala Ser Arg Glu
275 280 285

10 ACA AAC AAC AGC CTT ACC TTC GGG CCT GAA GAA GCA TTA GCT GAA CAG 1154
Thr Asn Asn Ser Leu Thr Phe Gly Pro Glu Glu Ala Leu Ala Glu Gln
290 295 300

15 ACC GTC TTC CTT TAGTTCTTCT CTGTCCATGT GGGATACATG GTATTATGTG 1206
Thr Val Phe Leu
305

20 GCTCATGAGG TACAATCTTT CTTTCAGCAC CGTGCTAGCT GATCTTTCGG ACAACTTGAC 1266
ACAAGATAGA GTTAACTGGG AAGAGAAAGC CTTGAATGAG GATTTCTTTC CATCAGGAAG 1326
CTACGGGCAA GTTTGCTGGG CCTTTGATTG CTTGATGACT GAAGTGGAAA GGCTGAGCCC 1386

25 ACTGTGGGTG GTGCTAGCCC TGGGCAGGGG CAGGTGACCC TGGGTGGTAT AAGAAAAGA 1446
GCTGTCACTA AAAGGAGAGG TGCCTAGTCT TACTGCAACT TGATATGTCA TGTTTGGTTG 1506
GTGTCTGTGG GAGGCCTGCC CTTTTCTGAA GAGAAGTGGT GGGAGAGTGG ATGGGGTGGG 1566
GGCAGAGGAA AAGTGGGGGA GAGGGCCTGG GAGGAGAGGA GGGAGGGGGA CGGGGTGGGG 1626
GTGGGGAAAA CTATGGTTGG GATGTAAAAA CGGATAATAA TATAAATATT AAATAAAAAG 1686

30 AGAGTATTGA GCGGTCTCAT CTACCATTG CAACTGACCT CTTCTGCAAA GGAATTCAGA 1746
AACCTAGCAC TACCCTGGCT CTGCAAACAC GGTTCCTCTAG GTGAAGCCTC TGCAGTGATT 1806
TGCAGAAGTA CTCAGACGAA TGAACCACAG TAGTTCTGCT GTTCTGAGG ACGTAGTTTA 1866
GAGACTGAAT TCTTTGGAAA GGACATAGGG ACAGTTTGCA CATTTGCTTG CACATCACAC 1926
ACACACACAC ACACACACAC ACACACACAC ACACACACAC ACACACACAC ACACACACAC 1986

40 TCTCTCTCTC TCTCTCTCTC GATACCTTAG GATAGGGTTC TACCCTGTTG CTCAGTGACA 2046
AAGAATCACT CTGTGGCGGA GGCAGGCTTC AAGCTTGACG CAATCCTCCT GCACCAGTTT 2106
CCTGAGTGCC AGACTTCCAG GTGTAAGCTA TGGCACTTAG CAGAACACTA GCTGAATCAA 2166
TGAAGACACT GAGGTTCCAA GAGGGAACCT GAATTATGAA GGTGAGTCAG AATCCAGATT 2226
TCCTGGCTCT ACCACTCTTA ACCTGTATCT GTTAGACCCC AAGCTCTGAG CTCATAGACA 2286

50 AGCTAATTTA AAATGCTTTT TAATAAGCAG AAGGCTCAGT TAGTACGGGG TTCAGGATAC 2346
TGCTTACTGG CAATATTTGA CTAGCCTCTA TTTTGTFTGT TTTTAAAGG CCTACTGACT 2406
GTAGTGTAAT TTGTAGGAAA CATGTTGCTA TGTATACCCA TTTGAGGGTA ATAAAAATGT 2466

55 TGGTAATTTT CAGCCAGCAC TTTCCAGGTA TTTCCCTTTT TATCCTTCAT 2516

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 818 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 1..138

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GGT CTC ATC TAC CAT TTG CAA CTG ACC TCT TCT GCA AAG GAC TTC AGA 48
Gly Leu Ile Tyr His Leu Gln Leu Thr Ser Ser Ala Lys Asp Phe Arg
1 5 10 15

AAC CTA GCA CTA CCC TGG CTC TGC AAA CAC GGT TCT CTA GGT GAA GCC 96
Asn Leu Ala Leu Pro Trp Leu Cys Lys His Gly Ser Leu Gly Glu Ala
20 25 30

TCT GCA GTG ATT TGC AGA AGT ACT CAG ACG AAT GAA CCA CAG 138
Ser Ala Val Ile Cys Arg Ser Thr Gln Thr Asn Glu Pro Gln
35 40 45

TAGTTCTGCT GTTCTGAGG ACGTAGTTTA GAGACTGAAT TCTTTGGAAA GGACATAGGG 198

ACAGTTTGCA CATTTGCTTG CACATCACAC ACACACACAC ACACACACAC ACACACACAC 258

ACACACACAC ACACACACAC ACACACACAC TCTCTCTCTC TCTCTCTCTC GATACCTTAG 318

GATAGGGTTC TACCCTGTTG CTCAGTGACA AAGAATCACT CTGTGGCGGA GGCAGGCTTC 378

AAGCTTGCAG CAATCCTCCT GCACCAGTTT CCTGAGTGCC AGACTTCCAG GTGTAAGCTA 438

TGGCACTTAG CAGAACACTA GCTGAATCAA TGAAGACACT GAGGTTCCAA GAGGGAACCT 498

GAATTATGAA GGTGAGTCAG AATCCAGATT TCCTGGCTCT ACCACTCTTA ACCTGTATCT 558

GTTAGACCCC AAGCTCTGAG CTCATAGACA AGCTAATTTA AAATGCTTTT TAATAAGCAG 618

AAGGCTCAGT TAGTACGGGG TTCAGGATAC TGCTTACTGG CAATATTGTA CTAGCCTCTA 678

TTTTGTTTGT TTTTAAAGG CCTACTGACT GTAGTGTAAT TTGTAGGAAA CATGTTGCTA 738

TGTATACCCA TTTGAGGGTA ATAAAAATGT TGGTAATTTT CAGCCAGCAC TTTCCAGGTA 798

TTTCCCTTTT TATCCTTCAT 818

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
(B) TYPE: amino acid

ACTTTATGGA AGAAAAAAGA AAAGATAGAC AAGCCTCTTC ATGTAATACC CCATAGTCTC 1020
AATAAGTGGT GTTCGTAACG TGGCTTCTCT TTCCTTACCT TTTACTGGTA GATTTCTCGG 1080
TTGATTGATG TCCCTGTAGG ACTTACTGGG TTTAAGATTG TTGGTTTCCT GTTTTAAGAT 1140
ATAAAGAAAC CATTTCCTAA CTAAAACACT GCCTTGACAA AATATACTTT TGGCAGTCAC 1200
TCTGTGTCCA GAATGGAATT TAAGCTTTCA TGGCCTAGCT GCTAGTGAAG GTTCTTTGCT 1260
TTTTTTTGGC TGTTGTATGT GAAATGGGGT TGGGTGGGAA CCACCTCACT GTGTTCTAGT 1320
GTTAGTCACC CCACCCCCGC AAGCAGAATC CTTTACCCA GCTTTTTCAC CCAGCTGTGC 1380
TCACCCGGTG CTCAGAACAG GCCTGGACAA GTCAGCTCCC CTAGAGTTCT GGGGACCTTT 1440
GAGTTGCCCT CATGGCCACA CCCTGATTCA GAACTCTCAC TCTGTCGTAA GATAGAGCTA 1500
CTGGGGAGTT TTATACCTCA ATAGACTCTT ACTAGTTTCT CTTTTCAGG TTGTGAAACT 1560
CAACCTTCAA AGACACTCTG TTCCATTCTT GTGGACTAAT AGGATCATCT TTAGCATCTG 1620
CCGGGTGGAT GCCATCCAGG CTTCTTTTTC TACATCTCTG TTTCTCGATT TTTGTGAGCC 1680
TAGGAGGTGC CTAAGCTCCA TTGGCTCTAG ATTCCTGGCT TTCCCCATCA TGTCTCCAA 1740
AGCATCTGAA GCT 1753

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TGTCCAGGCA GAGCTAGTGG CTGCCCCTAG CGCTTCCTCT TCTTTGATAC CCCAAAGTCT 60
GAGTTTATTA CACATCCTTG GTGACCAAAT CACATGGGAG CTTCTCCGA GGTCTTAGTA 120
AAGGGAAGTT GGAAAGGGGA AATTCCTGCC CCCCTGCC 158

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1398 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS

(B) LOCATION: 249..848

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

5 GAGTTTTATA CCTCAATAGA CTCTTACTAG TTTCTCTTTT TCAGGTTGTG AAACCTCAACC 60
 TTCAAAGACA CTCTGTTCCA TTTCTGTGGA CTAATAGGAT CATCTTTAGC ATCTGCCGGG 120
 10 TGGATGCCAT CCAGGCTTCT TTTTCTACAT CTCTGTTTCT CGATTTTGTG GAGCCTAGGA 180
 GGTGCCTAAG CTCCATTGGC TCTAGATTCC TGGCTTTCCC CATCATGTTT TCCAAAGCAT 240
 15 CTGAAGCT ATG GCT TGC AAT TGT CAG TTG ATG CAG GAT ACA CCA CTC CTC 290
 Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu
 1 5 10
 AAG TTT CCA TGT CCA AGG CTC AAT CTT CTC TTT GTG CTG CTG ATT CGT 338
 Lys Phe Pro Cys Pro Arg Leu Asn Leu Leu Phe Val Leu Leu Ile Arg
 20 15 20 25 30
 CTT TCA CAA GTG TCT TCA GCT GAC TTC TCT ACC CGC AAC ATA ACT GAG 386
 Leu Ser Gln Val Ser Ser Ala Asp Phe Ser Thr Pro Asn Ile Thr Glu
 35 40 45
 25 TCT GGA AAC CCA TCT GCA GAC ACT AAA AGG ATT ACC TGC TTT GCT TCC 434
 Ser Gly Asn Pro Ser Ala Asp Thr Lys Arg Ile Thr Cys Phe Ala Ser
 50 55 60
 30 GGG GGT TTC CCA AAG CCT CGC TTC TCT TGG TGG GAA AAT GGA AGA GAA 482
 Gly Gly Phe Pro Lys Pro Arg Phe Ser Trp Trp Glu Asn Gly Arg Glu
 65 70 75
 35 TTA CCT GGC ATC AAT ACG ACA ATT TCC CAG GAT CCT GAA TCT GAA TTG 530
 Leu Pro Gly Ile Asn Thr Thr Ile Ser Gln Asp Pro Glu Ser Glu Leu
 80 85 90
 TAC ACC ATT AGT AGC CAA CTA GAT TTC AAT ACG ACT CGC AAC CAC ACC 578
 Tyr Thr Ile Ser Ser Gln Leu Asp Phe Asn Thr Thr Arg Asn His Thr
 40 95 100 105 110
 ATT AAG TGT CTC ATT AAA TAT GGA GAT GCT CAC GTG TCA GAG GAC TTC 626
 Ile Lys Cys Leu Ile Lys Tyr Gly Asp Ala His Val Ser Glu Asp Phe
 115 120 125
 45 ACC TGG GAA AAA CCC CCA GAA GAC CCT CCT GAT AGC AAG AAC ACA CTT 674
 Thr Trp Glu Lys Pro Pro Glu Asp Pro Pro Asp Ser Lys Asn Thr Leu
 130 135 140
 50 GTG CTC TTT GGG GCA GGA TTC GGC GCA GTA ATA ACA GTC GTC GTC ATC 722
 Val Leu Phe Gly Ala Gly Phe Gly Ala Val Ile Thr Val Val Val Ile
 145 150 155
 55 GTT GTC ATC ATC AAA TGC TTC TGT AAG CAC AGA AGC TGT TTC AGA AGA 770
 Val Val Ile Ile Lys Cys Phe Cys Lys His Arg Ser Cys Phe Arg Arg
 160 165 170

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AAT GAG GCA AGC AGA GAA ACA AAC AAC AGC CTT ACC TTC GGG CCT GAA 818
 Asn Glu Ala Ser Arg Glu Thr Asn Asn Ser Leu Thr Phe Gly Pro Glu
 175 180 185 190
 5 GAA GCA TTA GCT GAA CAG ACC GTC TTC CTT TAGTTCTTCT CTGTCCATGT 868
 Glu Ala Leu Ala Glu Gln Thr Val Phe Leu
 195 200
 10 GGGATACATG GTATTATGTG GCTCATGAGG TACAATCTTT CTTTCAGCAC CGTGCTAGCT 928
 GATCTTTCGG ACAACTTGAC ACAAGATAGA GTTAACTGGG AAGAGAAAGC CTTGAATGAG 988
 GATTTCTTTC CATCAGGAAG CTACGGGCAA GTTTGCTGGG CCTTTGATTG CTTGATGACT 1048
 15 GAAGTGGAAG GGCTGAGCCC ACTGTGGGTG GTGCTAGCCC TGGGCAGGGG CAGGTGACCC 1108
 TGGGTGGTAT AAGAAAAAGA GCTGTCACTA AAAGGAGAGG TGCCTAGTCT TACTGCAACT 1168
 20 TGATATGTCA TGTTTGTTG GTGTCTGTGG GAGGCCTGCC CTTTCTGAA GAGAAGTGGT 1228
 GGGAGAGTGG ATGGGGTGGG GGCAGAGGAA AAGTGGGGGA GAGGCCTGG GAGGAGAGGA 1288
 GGGAGGGGGA CGGGGTGGGG GTGGGGAAAA CTATGGTTGG GATGTAAAAA CGGATAATAA 1348
 25 TATAAATATT AAATAAAAAG AGAGTATTGA GCAAAAAAAA AAAAAAAA 1398

(2) INFORMATION FOR SEQ ID NO:9:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 200 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

40 Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu Lys Phe
 1 5 10 15
 Pro Cys Pro Arg Leu Ile Leu Leu Phe Val Leu Leu Ile Arg Leu Ser
 20 25 30
 45 Gln Val Ser Ser Ala Asp Phe Ser Thr Pro Asn Ile Thr Glu Ser Gly
 35 40 45
 Asn Pro Ser Ala Asp Thr Lys Arg Ile Thr Cys Phe Ala Ser Gly Gly
 50 55 60
 Phe Pro Lys Pro Arg Phe Ser Trp Leu Glu Asn Gly Arg Glu Leu Pro
 65 70 75 80
 55 Gly Ile Asn Thr Thr Ile Ser Gln Asp Pro Glu Ser Glu Leu Tyr Thr
 85 90 95
 Ile Ser Ser Gln Leu Asp Phe Asn Thr Thr Arg Asn His Thr Ile Lys
 100 105 110

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Cys Leu Ile Lys Tyr Gly Asp Ala His Val Ser Glu Asp Phe Thr Trp
115 120 125

Glu Lys Pro Pro Glu Asp Pro Pro Asp Ser Lys Asn Thr Leu Val Leu
130 135 140

Phe Gly Ala Gly Phe Gly Ala Val Ile Thr Val Val Val Ile Val Val
145 150 155 160

Ile Ile Lys Cys Phe Cys Lys His Arg Ser Cys Phe Arg Arg Asn Glu
165 170 175

Ala Ser Arg Glu Thr Asn Asn Ser Leu Thr Phe Gly Pro Glu Glu Ala
180 185 190

Leu Ala Glu Gln Thr Val Phe Leu
195 200

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1570 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 249..890

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GAGTTTATA CCTCAATAGA CTCTTACTAG TTTCTCTTTT TCAGGTTGTG AAACCTCAACC 60
TTCAAAGACA CTCTGTTCCA TTTCTGTGGA CTAATAGGAT CATCTTTAGC ATCTGCCGGG 120
TGGATGCCAT CCAGGCTTCT TTTTCTACAT CTCTGTTTCT CGATTTTGTG GAGCCTAGGA 180
GGTGCCTAAG CTCCATTGGC TCTAGATTCC TGGCTTTCCC CATCATGTTC TCCAAAGCAT 240
CTGAAGCT ATG GCT TGC AAT TGT CAG TTG ATG CAG GAT ACA CCA CTC CTC 290
Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu
1 5 10
AAG TTT CCA TGT CCA AGG CTC AAT CTT CTC TTT GTG CTG CTG ATT CGT 338
Lys Phe Pro Cys Pro Arg Leu Asn Leu Leu Phe Val Leu Leu Ile Arg
15 20 25 30
CTT TCA CAA GTG TCT TCA GCT GAC TTC TCT ACC CCC AAC ATA ACT GAG 386
Leu Ser Gln Val Ser Ser Ala Asp Phe Ser Thr Pro Asn Ile Thr Glu
35 40 45
TCT GGA AAC CCA TCT GCA GAC ACT AAA AGG ATT ACC TGC TTT GCT TCC 434
Ser Gly Asn Pro Ser Ala Asp Thr Lys Arg Ile Thr Cys Phe Ala Ser
50 55 60

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Sub
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5	GGG GGT TTC CCA AAG CCT CGC TTC TCT TGG TTG GAA AAT GGA AGA GAA Gly Gly Phe Pro Lys Pro Arg Phe Ser Trp Leu Glu Asn Gly Arg Glu 65 70 75	482
10	TTA CCT GGC ATC AAT ACG ACA ATT TCC CAG GAT CCT GAA TCT GAA TTG Leu Pro Gly Ile Asn Thr Thr Ile Ser Gln Asp Pro Glu Ser Glu Leu 80 85 90	530
15	TAC ACC ATT AGT AGC CAA CTA GAT TTC AAT ACG ACT CGC AAC CAC ACC Tyr Thr Ile Ser Ser Gln Leu Asp Phe Asn Thr Thr Arg Asn His Thr 95 100 105 110	578
20	ATT AAG TGT CTC ATT AAA TAT GGA GAT GCT CAC GTG TCA GAG GAC TTC Ile Lys Cys Leu Ile Lys Tyr Gly Asp Ala His Val Ser Glu Asp Phe 115 120 125	626
25	ACC TGG GAA AAA CCC CCA GAA GAC CCT CCT GAT AGC AAG AAC ACA CTT Thr Trp Glu Lys Pro Pro Glu Asp Pro Pro Asp Ser Lys Asn Thr Leu 130 135 140	674
30	GTG CTC TTT GGG GCA GGA TTC GGC GCA GTA ATA ACA GTC GTC GTC ATC Val Leu Phe Gly Ala Gly Phe Gly Ala Val Ile Thr Val Val Val Ile 145 150 155	722
35	GTT GTC ATC ATC AAA TGC TTC TGT AAG CAC GGT CTC ATC TAC CAT TTG Val Val Ile Ile Lys Cys Phe Cys Lys His Gly Leu Ile Tyr His Leu 160 165 170	770
40	CAA CTG ACC TCT TCT GCA AAG GAC TTC AGA AAC CTA GCA CTA CCC TGG Gln Leu Thr Ser Ser Ala Lys Asp Phe Arg Asn Leu Ala Leu Pro Trp 175 180 185 190	818
45	CTC TGC AAA CAC GGT TCT CTA GGT GAA GCC TCT GCA GTG ATT TGC AGA Leu Cys Lys His Gly Ser Leu Gly Glu Ala Ser Ala Val Ile Cys Arg 195 200 205	866
50	AGT ACT CAG ACG AAT GAA CCA CAG TAGTTCTGCT GTTTCTGAGG ACGTAGTTTA Ser Thr Gln Thr Asn Glu Pro Gln 210	920
55	GAGACTGAAT TCTTTGGAAA GGACATAGGG ACAGTTTGCA CATTTGCTTG CACATCACAC ACACACACAC ACACACACAC ACACACACAC ACACACACAC ACACACACAC ACACACACAC TCTCTCTCTC TCTCTCTCTC GATACCTTAG GATAGGGTTC TACCCTGTTG CTCAGTGACA AAGAATCACT CTGTGGCGGA GGCAGGCTTC AAGCTTGCAG CAATCCTCCT GCACCAGTTT CCTGAGTGCC AGACTTCCAG GTGTAAGCTA TGGCACTTAG CAGAACACTA GCTGAATCAA TGAAGACACT GAGGTTCCAA GAGGGAACCT GAATTATGAA GGTGAGTCAG AATCCAGATT TCCTGGCTCT ACCACTCTTA ACCTGTATCT GTTAGACCCC AAGCTCTGAG CTCATAGACA AGCTAATTTA AAATGCTTTT TAATAAGCAG AAGGCTCAGT TAGTACGGGG TTCAGGATAC TGCTTACTGG CAATATTTGA CTAGCCTCTA TTTTGTGTGT TTTTAAAGG CCTACTGACT	980 1040 1100 1160 1220 1280 1340 1400 1460

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GTAGTGTAAAT TTGTAGGAAA CATGTTGCTA TGTATACCCA TTGAGGGTA ATAAAAATGT 1520
 TGGTAATTTT CAGCCAGCAC TTTCCAGGTA TTTCCCTTTT TATCCTTCAT 1570

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 214 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu Lys Phe
 1 5 10 15
 Pro Cys Pro Arg Leu Ile Leu Leu Phe Val Leu Leu Ile Arg Leu Ser
 20 25 30
 Gln Val Ser Ser Ala Asp Phe Ser Thr Pro Asn Ile Thr Glu Ser Gly
 35 40 45
 Asn Pro Ser Ala Asp Thr Lys Arg Ile Thr Cys Phe Ala Ser Gly Gly
 50 55 60
 Phe Pro Lys Pro Arg Phe Ser Trp Leu Glu Asn Gly Arg Glu Leu Pro
 65 70 75 80
 Gly Ile Asn Thr Thr Ile Ser Gln Asp Pro Glu Ser Glu Leu Tyr Thr
 85 90 95
 Ile Ser Ser Gln Leu Asp Phe Asn Thr Thr Arg Asn His Thr Ile Lys
 100 105 110
 Cys Leu Ile Lys Tyr Gly Asp Ala His Val Ser Glu Asp Phe Thr Trp
 115 120 125
 Glu Lys Pro Pro Glu Asp Pro Pro Asp Ser Lys Asn Thr Leu Val Leu
 130 135 140
 Phe Gly Ala Gly Phe Gly Ala Val Ile Thr Val Val Val Ile Val Val
 145 150 155 160
 Ile Ile Lys Cys Phe Cys Lys His Gly Leu Ile Tyr His Leu Gln Leu
 165 170 175
 Thr Ser Ser Ala Lys Asp Phe Arg Asn Leu Ala Leu Pro Trp Leu Cys
 180 185 190
 Lys His Gly Ser Leu Gly Glu Ala Ser Ala Val Ile Cys Arg Ser Thr
 195 200 205
 Gln Thr Asn Glu Pro Gln
 210

(2) INFORMATION FOR SEQ ID NO:12:

08702525-083095

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1261 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 194..1135

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

AGNCCCNAGA TTATTTCTCC CTGTATAAGG GACGCCCAGG AGGCCTGGGG AGCGGACAAG 60
 GCTCCTTTTA CTTTCTTCT TCTTCTATTT TTTTACGTT CTATTTTTTTT CTTTCATGTTT 120
 CTGTGATCTT CGGGAATGCT GCTGTGCTTG TGTGTGTGGT CCCTGAGCGC CGAGGTGGAG 180
 AGGCACTGGT GAC ATG TAT GTC ATC AAG ACA TGT GCA ACC TGC ACC ATG 229
 Met Tyr Val Ile Lys Thr Cys Ala Thr Cys Thr Met
 1 5 10
 GGC TTG GCA ATC CTT ATC TTT GTG ACA GTC TTG CTG ATC TCA GAT GCT 277
 Gly Leu Ala Ile Leu Ile Phe Val Thr Val Leu Leu Ile Ser Asp Ala
 15 20 25
 GTT TCC GTG GAG ACG CAA GCT TAT TTC AAT GGG ACT GCA TAT CTG CCG 325
 Val Ser Val Glu Thr Gln Ala Tyr Phe Asn Gly Thr Ala Tyr Leu Pro
 30 35 40
 TGC CCA TTT ACA AAG GCT CAA AAC ATA AGC CTG AGT GAG CTG GTA GTA 373
 Cys Pro Phe Thr Lys Ala Gln Asn Ile Ser Leu Ser Glu Leu Val Val
 45 50 55 60
 TTT TGG CAG GAC CAG CAA AAG TTG GTT CTG TAC GAG CAC TAT TTG GGC 421
 Phe Trp Gln Asp Gln Gln Lys Leu Val Leu Tyr Glu His Tyr Leu Gly
 65 70 75
 ACA GAG AAA CTT GAT AGT GTG AAT GCC AAG TAC CTG GGC CGC ACG AGC 469
 Thr Glu Lys Leu Asp Ser Val Asn Ala Lys Tyr Leu Gly Arg Thr Ser
 80 85 90
 TTT GAC AGG AAC AAC TGG ACT CTA CGA CTT CAC AAT GTT CAG ATC AAG 517
 Phe Asp Arg Asn Asn Trp Thr Leu Arg Leu His Asn Val Gln Ile Lys
 95 100 105
 GAC ATG GGC TCG TAT GAT TGT TTT ATA CAA AAA AAG CCA CCC ACA GGA 565
 Asp Met Gly Ser Tyr Asp Cys Phe Ile Gln Lys Lys Pro Pro Thr Gly
 110 115 120
 TCA ATT ATC CTC CAA CAG ACA TTA ACA GAA CTG TCA GTG ATC GCC AAC 613
 Ser Ile Ile Leu Gln Gln Thr Leu Thr Glu Leu Ser Val Ile Ala Asn
 125 130 135 140

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	TTC AGT GAA CCT GAA ATA AAA CTG GCT CAG AAT GTA ACA GGA AAT TCT	661
	Phe Ser Glu Pro Glu Ile Lys Leu Ala Gln Asn Val Thr Gly Asn Ser	
	145 150 155	
5	GGC ATA AAT TTG ACC TGC ACG TCT AAG CAA GGT CAC CCG AAA CCT AAG	709
	Gly Ile Asn Leu Thr Cys Thr Ser Lys Gln Gly His Pro Lys Pro Lys	
	160 165 170	
10	AAG ATG TAT TTT CTG ATA ACT AAT TCA ACT AAT GAG TAT GGT GAT AAC	757
	Lys Met Tyr Phe Leu Ile Thr Asn Ser Thr Asn Glu Tyr Gly Asp Asn	
	175 180 185	
15	ATG CAG ATA TCA CAA GAT AAT GTC ACA GAA CTG TTC AGT ATC TCC AAC	805
	Met Gln Ile Ser Gln Asp Asn Val Thr Glu Leu Phe Ser Ile Ser Asn	
	190 195 200	
20	AGC CTC TCT CTT TCA TTC CCG GAT GGT GTG TGG GAT ATG ACC GTT GTG	853
	Ser Leu Ser Leu Ser Phe Pro Asp Gly Val Trp His Met Thr Val Val	
	205 210 215 220	
25	TGT GTT CTG GAA ACG GAG TCA ATG AAG ATT TCC TCC AAA CCT CTC AAT	901
	Cys Val Leu Glu Thr Glu Ser Met Lys Ile Ser Ser Lys Pro Leu Asn	
	225 230 235	
30	TTC ACT CAA GAG TTT CCA TCT CCT CAA ACG TAT TGG AAG GAG ATT ACA	949
	Phe Thr Gln Glu Phe Pro Ser Pro Gln Thr Tyr Trp Lys Glu Ile Thr	
	240 245 250	
35	GCT TCA GTT ACT GTG GCC CTC CTC CTT GTG ATG CTG CTC ATC ATT GTA	997
	Ala Ser Val Thr Val Ala Leu Leu Leu Val Met Leu Leu Ile Ile Val	
	255 260 265	
40	TGT CAC AAG AAG CCG AAT CAG CCT AGC AGG CCC AGC AAC ACA GCC TCT	1045
	Cys His Lys Lys Pro Asn Gln Pro Ser Arg Pro Ser Asn Thr Ala Ser	
	270 275 280	
45	AAG TTA GAG CGG GAT AGT AAC GCT GAC AGA GAG ACT ATC AAC CTG AAG	1093
	Lys Leu Glu Arg Asp Ser Asn Ala Asp Arg Glu Thr Ile Asn Leu Lys	
	285 290 295 300	
50	GAA CTT GAA CCC CAA ATT GCT TCA GCA AAA CCA AAT GCA GAG	1135
	Glu Leu Glu Pro Gln Ile Ala Ser Ala Lys Pro Asn Ala Glu	
	305 310	
55	TGAAGGCAGT GAGAGCCTGA GGAAAGAGTT AAAAATTGCT TTGCCTGAAA TAAGAAGTGC	1195
	AGAGTTTCTC AGAATTCAAA AATGTTCTCA GCTGATTGGA ATTCTACAGT TGAATAATTA	1255
	AAGAAC	1261

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

5 Met Tyr Val Ile Lys Thr Cys Ala Thr Cys Thr Met Gly Leu Ala Ile
 1 5 10 15
 Leu Ile Phe Val Thr Val Leu Leu Ile Ser Asp Ala Val Ser Val Glu
 20 25 30
 10 Thr Gln Ala Tyr Phe Asn Gly Thr Ala Tyr Leu Pro Cys Pro Phe Thr
 35 40 45
 Lys Ala Gln Asn Ile Ser Leu Ser Glu Leu Val Val Phe Trp Gln Asp
 50 55 60
 15 Gln Gln Lys Leu Val Leu Tyr Glu His Tyr Leu Gly Thr Glu Lys Leu
 65 70 75 80
 20 Asp Ser Val Asn Ala Lys Tyr Leu Gly Arg Thr Ser Phe Asp Arg Asn
 85 90 95
 Asn Trp Thr Leu Arg Leu His Asn Val Gln Ile Lys Asp Met Gly Ser
 100 105 110
 25 Tyr Asp Cys Phe Ile Gln Lys Lys Pro Pro Thr Gly Ser Ile Ile Leu
 115 120 125
 Gln Gln Thr Leu Thr Glu Leu Ser Val Ile Ala Asn Phe Ser Glu Pro
 130 135 140
 30 Glu Ile Lys Leu Ala Gln Asn Val Thr Gly Asn Ser Gly Ile Asn Leu
 145 150 155 160
 35 Thr Cys Thr Ser Lys Gln Gly His Pro Lys Pro Lys Lys Met Tyr Phe
 165 170 175
 Leu Ile Thr Asn Ser Thr Asn Glu Tyr Gly Asp Asn Met Gln Ile Ser
 180 185 190
 40 Gln Asp Asn Val Thr Glu Leu Phe Ser Ile Ser Asn Ser Leu Ser Leu
 195 200 205
 Ser Phe Pro Asp Gly Val Trp His Met Thr Val Val Cys Val Leu Glu
 210 215 220
 45 Thr Glu Ser Met Lys Ile Ser Ser Lys Pro Leu Asn Phe Thr Gln Glu
 225 230 235 240
 50 Phe Pro Ser Pro Gln Thr Tyr Trp Lys Glu Ile Thr Ala Ser Val Thr
 245 250 255
 Val Ala Leu Leu Leu Val Met Leu Leu Ile Ile Val Cys His Lys Lys
 260 265 270
 55 Pro Asn Gln Pro Ser Arg Pro Ser Asn Thr Ala Ser Lys Leu Glu Arg
 275 280 285
 Asp Ser Asn Ala Asp Arg Glu Thr Ile Asn Leu Lys Glu Leu Glu Pro
 290 295 300

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Gln Ile Ala Ser Ala Lys Pro Asn Ala Glu
305 310

5 (2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 223 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 194..223

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AGNCCCNAGA TTATTTCTCC CTGTATAAGG GACGCCCAGG AGGCCTGGGG AGCGGACAAG 60
25 GCTCCTTTTA CTTTCTTCT TCTTCTATTT TTTTACCTT CTATTTTTTTT CTTTCATGTTT 120
CTGTGATCTT CGGGAATGCT GCTGTGCTTG TGTGTGTGGT CCCTGAGCGC CGAGGTGGAG 180
AGGCACTGGT GAC ATG TAT GTC ATC AAG ACA TGT GCA ACC TGC 223
Met Tyr Val Ile Lys Thr Cys Ala Thr Cys
1 5 10

35 (2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

45 Met Tyr Val Ile Lys Thr Cys Ala Thr Cys
1 5 10

(2) INFORMATION FOR SEQ ID NO:16:

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1716 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
55 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

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301

(A) NAME/KEY: CDS

(B) LOCATION: 249..1166

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GAGTTTATA CCTCAATAGA CTCTTACTAG TTTCTCTTTT TCAGGTTGTG AAACCTCAACC 60
 TTCAAAGACA CTCTGTTCCA TTTCTGTGGA CTAATAGGAT CATCTTTAGC ATCTGCCGGG 120
 TGGATGCCAT CCAGGCTTCT TTTTCTACAT CTCTGTTTCT CGATTTTGTG GAGCCTAGGA 180
 GGTGCCTAAG CTCCATTGGC TCTAGATTCC TGGCTTTCCC CATCATGTTT TCCAAAGCAT 240
 15 CTGAAGCT ATG GCT TGC AAT TGT CAG TTG ATG CAG GAT ACA CCA CTC CTC 290
 Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu
 1 5 10
 AAG TTT CCA TGT CCA AGG CTC AAT CTT CTC TTT GTG CTG CTG ATT CGT 338
 20 Lys Phe Pro Cys Pro Arg Leu Asn Leu Leu Phe Val Leu Leu Ile Arg
 15 20 25 30
 CTT TCA CAA GTG TCT TCA GAT GTT GAT GAA CAA CTG TCC AAG TCA GTG 386
 25 Leu Ser Gln Val Ser Ser Asp Val Asp Glu Gln Leu Ser Lys Ser Val
 35 40 45
 AAA GAT AAG GTA TTG CTG CCT TGC CGT TAC AAC TCT CCT CAT GAA GAT 434
 Lys Asp Lys Val Leu Leu Pro Cys Arg Tyr Asn Ser Pro His Glu Asp
 50 55 60
 GAG TCT GAA GAC CGA ATC TAC TGG CAA AAA CAT GAC AAA GTG GTG CTG 482
 30 Glu Ser Glu Asp Arg Ile Tyr Trp Gln Lys His Asp Lys Val Val Leu
 65 70 75
 TCT GTC ATT GCT GGG AAA CTA AAA GTG TGG CCC GAG TAT AAG AAC CGG 530
 35 Ser Val Ile Ala Gly Lys Leu Lys Val Trp Pro Glu Tyr Lys Asn Arg
 80 85 90
 ACT TTA TAT GAC AAC ACT ACC TAC TCT CTT ATC ATC CTG GGC CTG GTC 578
 40 Thr Leu Tyr Asp Asn Thr Thr Tyr Ser Leu Ile Ile Leu Gly Leu Val
 95 100 105 110
 CTT TCA GAC CGG GGC ACA TAC AGC TGT GTC GTT CAA AAG AAG GAA AGA 626
 45 Leu Ser Asp Arg Gly Thr Tyr Ser Cys Val Val Gln Lys Lys Glu Arg
 115 120 125
 GGA ACG TAT GAA GTT AAA CAC TTG GCT TTA GTA AAG TTG TCC ATC AAA 674
 Gly Thr Tyr Glu Val Lys His Leu Ala Leu Val Lys Leu Ser Ile Lys
 130 135 140
 GCT GAC TTC TCT ACC CCC AAC ATA ACT GAG TCT GGA AAC CCA TCT GCA 722
 Ala Asp Phe Ser Thr Pro Asn Ile Thr Glu Ser Gly Asn Pro Ser Ala
 145 150 155
 GAC ACT AAA AGG ATT ACC TGC TTT GCT TCC GGG GGT TTC CCA AAG CCT 770
 55 Asp Thr Lys Arg Ile Thr Cys Phe Ala Ser Gly Gly Phe Pro Lys Pro
 160 165 170

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CGC TTC TCT TGG TTG GAA AAT GGA AGA GAA TTA CCT GGC ATC AAT ACG 818
 Arg Phe Ser Trp Leu Glu Asn Gly Arg Glu Leu Pro Gly Ile Asn Thr
 175 180 185 190

5 ACA ATT TCC CAG GAT CCT GAA TCT GAA TTG TAC ACC ATT AGT AGC CAA 866
 Thr Ile Ser Gln Asp Pro Glu Ser Glu Leu Tyr Thr Ile Ser Ser Gln
 195 200 205

10 CTA GAT TTC AAT ACG ACT CGC AAC CAC ACC ATT AAG TGT CTC ATT AAA 914
 Leu Asp Phe Asn Thr Thr Arg Asn His Thr Ile Lys Cys Leu Ile Lys
 210 215 220

15 TAT GGA GAT GCT CAC GTG TCA GAG GAC TTC ACC TGG GAA AAA CCC CCA 962
 Tyr Gly Asp Ala His Val Ser Glu Asp Phe Thr Trp Glu Lys Pro Pro
 225 230 235

20 GAA GAC CCT CCT GAT AGC AAG AAC ACA CTT GTG CTC TTT GGG GCA GGA 1010
 Glu Asp Pro Pro Asp Ser Lys Asn Thr Leu Val Leu Phe Gly Ala Gly
 240 245 250

TTC GGC GCA GTA ATA ACA GTC GTC GTC ATC GTT GTC ATC ATC AAA TGC 1058
 Phe Gly Ala Val Ile Thr Val Val Val Ile Val Val Ile Ile Lys Cys
 255 260 265 270

25 TTC TGT AAG CAC AGA AGC TGT TTC AGA AGA AAT GAG GCA AGC AGA GAA 1106
 Phe Cys Lys His Arg Ser Cys Phe Arg Arg Asn Glu Ala Ser Arg Glu
 275 280 285

30 ACA AAC AAC AGC CTT ACC TTC GGG CCT GAA GAA GCA TTA GCT GAA CAG 1154
 Thr Asn Asn Ser Leu Thr Phe Gly Pro Glu Glu Ala Leu Ala Glu Gln
 290 295 300

35 ACC GTC TTC CTT TAGTTCTTCT CTGTCCATGT GGGATACATG GTATTATGTG 1206
 Thr Val Phe Leu
 305

GCTCATGAGG TACAATCTTT CTTTCAGCAC CGTGCTAGCT GATCTTTCGG ACAACTTGAC 1266

40 ACAAGATAGA GTTAACTGGG AAGAGAAAGC CTTGAATGAG GATTTCTTTC CATCAGGAAG 1326

CTACGGGCAA GTTTGCTGGG CCTTTGATTG CTTGATGACT GAAGTGGAAA GGCTGAGCCC 1386

ACTGTGGGTG GTGCTAGCCC TGGGCAGGGG CAGGTGACCC TGGGTGGTAT AAGAAAAAGA 1446

45 GCTGTCACTA AAAGGAGAGG TGCCTAGTCT TACTGCAACT TGATATGTCA TGTTTGGTTG 1506

GTGTCTGTGG GAGGCCTGCC CTTTTCTGAA GAGAAGTGGT GGGAGAGTGG ATGGGGTGGG 1566

50 GGCAGAGGAA AAGTGGGGGA GAGGGCCTGG GAGGAGAGGA GGGAGGGGGA CGGGGTGGGG 1626

GTGGGGAAAA CTATGGTTGG GATGTAAAAA CGGATAATAA TATAAATATT AAATAAAAAG 1686

AGAGTATTGA GCAAAAAAAA AAAAAAAA 1716

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 306 amino acids

360680 52520280

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu Lys Phe
 1 5 10 15
 Pro Cys Pro Arg Leu Ile Leu Leu Phe Val Leu Leu Ile Arg Leu Ser
 20 25 30
 Gln Val Ser Ser Asp Val Asp Glu Gln Leu Ser Lys Ser Val Lys Asp
 35 40 45
 Lys Val Leu Leu Pro Cys Arg Tyr Asn Ser Pro His Glu Asp Glu Ser
 50 55 60
 Glu Asp Arg Ile Tyr Trp Gln Lys His Asp Lys Val Val Leu Ser Val
 65 70 75 80
 Ile Ala Gly Lys Leu Lys Val Trp Pro Glu Tyr Lys Asn Arg Thr Leu
 85 90 95
 Tyr Asp Asn Thr Thr Tyr Ser Leu Ile Ile Leu Gly Leu Val Leu Ser
 100 105 110
 Asp Arg Gly Thr Tyr Ser Cys Val Val Gln Lys Lys Glu Arg Gly Thr
 115 120 125
 Tyr Glu Val Lys His Leu Ala Leu Val Lys Leu Ser Ile Lys Ala Asp
 130 135 140
 Phe Ser Thr Pro Asn Ile Thr Glu Ser Gly Asn Pro Ser Ala Asp Thr
 145 150 155 160
 Lys Arg Ile Thr Cys Phe Ala Ser Gly Gly Phe Pro Lys Pro Arg Phe
 165 170 175
 Ser Trp Leu Glu Asn Gly Arg Glu Leu Pro Gly Ile Asn Thr Thr Ile
 180 185 190
 Ser Gln Asp Pro Glu Ser Glu Leu Tyr Thr Ile Ser Ser Gln Leu Asp
 195 200 205
 Phe Asn Thr Thr Arg Asn His Thr Ile Lys Cys Leu Ile Lys Tyr Gly
 210 215 220
 Asp Ala His Val Ser Glu Asp Phe Thr Trp Glu Lys Pro Pro Glu Asp
 225 230 235 240
 Pro Pro Asp Ser Lys Asn Thr Leu Val Leu Phe Gly Ala Gly Phe Gly
 245 250 255
 Ala Val Ile Thr Val Val Val Ile Val Val Ile Ile Lys Cys Phe Cys
 260 265 270

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Lys His Arg Ser Cys Phe Arg Arg Asn Glu Ala Ser Arg Glu Thr Asn
 275 280 285

Asn Ser Leu Thr Phe Gly Pro Glu Glu Ala Leu Ala Glu Gln Thr Val
 290 295 300

Phe Leu
 305

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1491 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 318..1181

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CCAAAGAAAA AGTGATTTGT CATTGCTTTA TAGACTGTAA GAAGAGAACA TCTCAGAAGT 60
 GGAGTCTTAC CCTGAAATCA AAGGATTTAA AGAAAAAGTG GAATTTTCTC TCAGCAAGCT 120
 GTGAAACTAA ATCCACAACC TTTGGAGACC CAGGAACACC CTCCAATCTC TGTGTGTTTT 180
 GTAAACATCA CTGGAGGGTC TTCTACGTGA GCAATTGGAT TGTCATCAGC CCTGCCTGTT 240
 TTGCACCTGG GAAGTGCCCT GGTCTTACTT GGGTCCAAAT TGTGCGCTTT CACTTTTGAC 300
 CCTAAGCATC TGAAGCC ATG GGC CAC ACA CGG AGG CAG GGA ACA TCA CCA 350
 Met Gly His Thr Arg Arg Gln Gly Thr Ser Pro
 1 5 10
 TCC AAG TGT CCA TAC CTG AAT TTC TTT CAG CTC TTG GTG CTG GCT GGT 398
 Ser Lys Cys Pro Tyr Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly
 15 20 25
 CTT TCT CAC TTC TGT TCA GGT GTT ATC CAC GTG ACC AAG GAA GTG AAA 446
 Leu Ser His Phe Cys Ser Gly Val Ile His Val Thr Lys Glu Val Lys
 30 35 40
 GAA GTG GCA ACG CTG TCC TGT GGT CAC AAT GTT TCT GTT GAA GAG CTG 494
 Glu Val Ala Thr Leu Ser Cys Gly His Asn Val Ser Val Glu Glu Leu
 45 50 55
 GCA CAA ACT CGC ATC TAC TGG CAA AAG GAG AAG AAA ATG GTG CTG ACT 542
 Ala Gln Thr Arg Ile Tyr Trp Gln Lys Glu Lys Lys Met Val Leu Thr
 60 65 70 75

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	ATG	ATG	TCT	GGG	GAC	ATG	AAT	ATA	TGG	CCC	GAG	TAC	AAG	AAC	CGG	ACC	590
	Met	Met	Ser	Gly	Asp	Met	Asn	Ile	Trp	Pro	Glu	Tyr	Lys	Asn	Arg	Thr	
				80						85					90		
5	ATC	TTT	GAT	ATC	ACT	AAT	AAC	CTC	TCC	ATT	GTG	ATC	CTG	GCT	CTG	CGC	638
	Ile	Phe	Asp	Ile	Thr	Asn	Asn	Leu	Ser	Ile	Val	Ile	Leu	Ala	Leu	Arg	
				95					100					105			
10	CCA	TCT	GAC	GAG	GGC	ACA	TAC	GAG	TGT	GTT	GTT	CTG	AAG	TAT	GAA	AAA	686
	Pro	Ser	Asp	Glu	Gly	Thr	Tyr	Glu	Cys	Val	Val	Leu	Lys	Tyr	Glu	Lys	
				110				115					120				
15	GAC	GCT	TTC	AAG	CGG	GAA	CAC	CTG	GCT	GAA	GTG	ACG	TTA	TCA	GTC	AAA	734
	Asp	Ala	Phe	Lys	Arg	Glu	His	Leu	Ala	Glu	Val	Thr	Leu	Ser	Val	Lys	
				125			130					135					
20	GCT	GAC	TTC	CCT	ACA	CCT	AGT	ATA	TCT	GAC	TTT	GAA	ATT	CCA	ACT	TCT	782
	Ala	Asp	Phe	Pro	Thr	Pro	Ser	Ile	Ser	Asp	Phe	Glu	Ile	Pro	Thr	Ser	
						145				150					155		
25	AAT	ATT	AGA	AGG	ATA	ATT	TGC	TCA	ACC	TCT	GGA	GGT	TTT	CCA	GAG	CCT	830
	Asn	Ile	Arg	Arg	Ile	Ile	Cys	Ser	Thr	Ser	Gly	Gly	Phe	Pro	Glu	Pro	
					160					165					170		
30	CAC	CTC	TCC	TGG	TTG	GAA	AAT	GGA	GAA	GAA	TTA	AAT	GCC	ATC	AAC	ACA	878
	His	Leu	Ser	Trp	Leu	Glu	Asn	Gly	Glu	Glu	Leu	Asn	Ala	Ile	Asn	Thr	
				175				180					185				
35	ACA	GTT	TCC	CAA	GAT	CCT	GAA	ACT	GAG	CTC	TAT	GCT	GTT	AGC	AGC	AAA	926
	Thr	Val	Ser	Gln	Asp	Pro	Glu	Thr	Glu	Leu	Tyr	Ala	Val	Ser	Ser	Lys	
				190				195					200				
40	CTG	GAT	TTC	AAT	ATG	ACA	ACC	AAC	CAC	AGC	TTC	ATG	TGT	CTC	ATC	AAG	974
	Leu	Asp	Phe	Asn	Met	Thr	Thr	Asn	His	Ser	Phe	Met	Cys	Leu	Ile	Lys	
				205			210				215						
45	TAT	GGA	CAT	TTA	AGA	GTG	AAT	CAG	ACC	TTC	AAC	TGG	AAT	ACA	ACC	AAG	1022
	Tyr	Gly	His	Leu	Arg	Val	Asn	Gln	Thr	Phe	Asn	Trp	Asn	Thr	Thr	Lys	
						225				230					235		
50	CAA	GAG	CAT	TTT	CCT	GAT	AAC	CTG	CTC	CCA	TCC	TGG	GCC	ATT	ACC	TTA	1070
	Gln	Glu	His	Phe	Pro	Asp	Asn	Leu	Leu	Pro	Ser	Trp	Ala	Ile	Thr	Leu	
					240					245					250		
55	ATC	TCA	GTA	AAT	GGA	ATT	TTT	GTG	ATA	TGC	TGC	CTG	ACC	TAC	TGC	TTT	1118
	Ile	Ser	Val	Asn	Gly	Ile	Phe	Val	Ile	Cys	Cys	Leu	Thr	Tyr	Cys	Phe	
				255				260						265			
60	GCC	CCA	AGA	TGC	AGA	GAG	AGA	AGG	AGG	AAT	GAG	AGA	TTG	AGA	AGG	GAA	1166
	Ala	Pro	Arg	Cys	Arg	Glu	Arg	Arg	Arg	Asn</							

AAGCTGAACA GTTACAAGAT GGCTGGCATC CCTCTCCTTT CTCCCCATAT GCAATTTGCT 1401
 TAATGTAACC TCTTCTTTTG CCATGTTTCC ATTCTGCCAT CTTGAATTGT CTTGTCAGCC 1461
 AATTCATTAT CTATTAAACA CTAATTTGAG 1491

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met Gly His Thr Arg Arg Gln Gly Thr Ser Pro Ser Lys Cys Pro Tyr
 1 5 10 15
 Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly Leu Ser His Phe Cys
 20 25 30
 Ser Gly Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu
 35 40 45
 Ser Cys Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile
 50 55 60
 Tyr Trp Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp
 65 70 75 80
 Met Asn Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr
 85 90 95
 Asn Asn Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly
 100 105 110
 Thr Tyr Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg
 115 120 125
 Glu His Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr
 130 135 140
 Pro Ser Ile Ser Asp Phe Glu Ile Pro Thr Ser Asn Ile Arg Arg Ile
 145 150 155 160
 Ile Cys Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu
 165 170 175
 Glu Asn Gly Glu Glu Leu Asn Ala Ile Asn Thr Thr Val Ser Gln Asp
 180 185 190
 Pro Glu Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met
 195 200 205

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Sub
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Thr Thr Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg
210 215 220

Val Asn Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro
225 230 235 240

Asp Asn Leu Leu Pro Ser Trp Ala Ile Thr Leu Ile Ser Val Asn Gly
245 250 255

Ile Phe Val Ile Cys Cys Leu Thr Tyr Cys Phe Ala Pro Arg Cys Arg
260 265 270

Glu Arg Arg Arg Asn Glu Arg Leu Arg Arg Glu Ser Val Arg Pro Val
275 280 285

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1151 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 99..1025

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

35 GGAGCAAGCA GACGCGTAAG AGTGGCTCCT GTAGGCAGCA CGGACTTGAA CAACCAGACT 60
CCTGTAGACG TGTTCCAGAA CTTACGGAAG CACCCACG ATG GAC CCC AGA TGC 113
Met Asp Pro Arg Cys
1 5
40 ACC ATG GGC TTG GCA ATC CTT ATC TTT GTG ACA GTC TTG CTG ATC TCA 161
Thr Met Gly Leu Ala Ile Leu Ile Phe Val Thr Val Leu Leu Ile Ser
10 15 20
45 GAT GCT GTT TCC GTG GAG ACG CAA GCT TAT TTC AAT GGG ACT GCA TAT 209
Asp Ala Val Ser Val Glu Thr Gln Ala Tyr Phe Asn Gly Thr Ala Tyr
25 30 35
50 CTG CCG TGC CCA TTT ACA AAG GCT CAA AAC ATA AGC CTG AGT GAG CTG 257
Leu Pro Cys Pro Phe Thr Lys Ala Gln Asn Ile Ser Leu Ser Glu Leu
40 45 50
55 GTA GTA TTT TGG CAG GAC CAG CAA AAG TTG GTT CTG TAC GAG CAC TAT 305
Val Val Phe Trp Gln Asp Gln Gln Lys Leu Val Leu Tyr Glu His Tyr
55 60 65
TTG GGC ACA GAG AAA CTT GAT AGT GTG AAT GCC AAG TAC CTG GGC CGC 353
Leu Gly Thr Glu Lys Leu Asp Ser Val Asn Ala Lys Tyr Leu Gly Arg
70 75 80 85

950330 52520/280

806
a1

ACG AGC TTT GAC AGG AAC AAC TGG ACT CTA CGA CTT CAC AAT GTT CAG 401
 Thr Ser Phe Asp Arg Asn Asn Trp Thr Leu Arg Leu His Asn Val Gln
 90 95 100
 5
 ATC AAG GAC ATG GGC TCG TAT GAT TGT TTT ATA CAA AAA AAG CCA CCC 449
 Ile Lys Asp Met Gly Ser Tyr Asp Cys Phe Ile Gln Lys Lys Pro Pro
 105 110 115
 10
 ACA GGA TCA ATT ATC CTC CAA CAG ACA TTA ACA GAA CTG TCA GTG ATC 497
 Thr Gly Ser Ile Ile Leu Gln Gln Thr Leu Thr Glu Leu Ser Val Ile
 120 125 130
 15
 GCC AAC TTC AGT GAA CCT GAA ATA AAA CTG GCT CAG AAT GTA ACA GGA 545
 Ala Asn Phe Ser Glu Pro Glu Ile Lys Leu Ala Gln Asn Val Thr Gly
 135 140 145
 20
 AAT TCT GGC ATA AAT TTG ACC TGC ACG TCT AAG CAA GGT CAC CCG AAA 593
 Asn Ser Gly Ile Asn Leu Thr Cys Thr Ser Lys Gln Gly His Pro Lys
 150 155 160 165
 25
 CCT AAG AAG ATG TAT TTT CTG ATA ACT AAT TCA ACT AAT GAG TAT GGT 641
 Pro Lys Lys Met Tyr Phe Leu Ile Thr Asn Ser Thr Asn Glu Tyr Gly
 170 175 180
 30
 GAT AAC ATG CAG ATA TCA CAA GAT AAT GTC ACA GAA CTG TTC AGT ATC 689
 Asp Asn Met Gln Ile Ser Gln Asp Asn Val Thr Glu Leu Phe Ser Ile
 185 190 195
 35
 TCC AAC AGC CTC TCT CTT TCA TTC CCG GAT GGT GTG TGG CAT ATG ACC 737
 Ser Asn Ser Leu Ser Leu Ser Phe Pro Asp Gly Val Trp His Met Thr
 200 205 210
 40
 GTT GTG TGT GTT CTG GAA ACG GAG TCA ATG AAG ATT TCC TCC AAA CCT 785
 Val Val Cys Val Leu Glu Thr Glu Ser Met Lys Ile Ser Ser Lys Pro
 215 220 225
 45
 CTC AAT TTC ACT CAA GAG TTT CCA TCT CCT CAA ACG TAT TGG AAG GAG 833
 Leu Asn Phe Thr Gln Glu Phe Pro Ser Pro Gln Thr Tyr Trp Lys Glu
 230 235 240 245
 50
 ATT ACA GCT TCA GTT ACT GTG GCC CTC CTC CTT GTG ATG CTG CTC ATC 881
 Ile Thr Ala Ser Val Thr Val Ala Leu Leu Leu Val Met Leu Leu Ile
 250 255 260
 55
 ATT GTA TGT CAC AAG AAG CCG AAT CAG CCT AGC AGG CCC AGC AAC ACA 929
 Ile Val Cys His Lys Lys Pro Asn Gln Pro Ser Arg Pro Ser Asn Thr
 265 270 275
 60
 GCC TCT AAG TTA GAG CGG GAT AGT AAC GCT GAC AGA GAG ACT ATC AAC 977
 Ala Ser Lys Leu Glu Arg Asp Ser Asn Ala Asp Arg Glu Thr Ile Asn
 280 285 290
 65
 CTG AAG GAA CTT GAA CCC CAA ATT GCT TCA GCA AAA CCA AAT GCA GAG 1025
 Leu Lys Glu Leu Glu Pro Gln Ile Ala Ser Ala Lys Pro Asn Ala Glu
 295 300 305
 TGAAGGCAGT GAGAGCCTGA GGAAAGAGTT AAAAATTGCT TTGCCTGAAA TAAGAAGTGC 1085

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Sub a1

AGAGTTTCTC AGAATTCAAA AATGTTCTCA GCTGATTGGA ATTCTACAGT TGAATAATTA 1145

AAGAAC 1151

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 309 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met Asp Pro Arg Cys Thr Met Gly Leu Ala Ile Leu Ile Phe Val Thr
1 5 10 15

20 Val Leu Leu Ile Ser Asp Ala Val Ser Val Glu Thr Gln Ala Tyr Phe
20 25 30

Asn Gly Thr Ala Tyr Leu Pro Cys Pro Phe Thr Lys Ala Gln Asn Ile
35 40 45

Ser Leu Ser Glu Leu Val Val Phe Trp Gln Asp Gln Gln Lys Leu Val
50 55 60

30 Leu Tyr Glu His Tyr Leu Gly Thr Glu Lys Leu Asp Ser Val Asn Ala
 65 70 75 80

Lys Tyr Leu Gly Arg Thr Ser Phe Asp Arg Asn Asn Trp Thr Leu Arg
85 90 95

35 Leu His Asn Val Gln Ile Lys Asp Met Gly Ser Tyr Asp Cys Phe Ile
 100 105 110

Gln Lys Lys Pro Pro Thr Gly Ser Ile Ile Leu Gln Gln Thr Leu Thr
115 120 125

Glu Leu Ser Val Ile Ala Asn Phe Ser Glu Pro Glu Ile Lys Leu Ala
130 135 140

45 Gln Asn Val Thr Gly Asn Ser Gly Ile Asn Leu Thr Cys Thr Ser Lys
 145 150 155 160

Gln Gly His Pro Lys Pro Lys Lys Met Tyr Phe Leu Ile Thr Asn Ser
165 170 175

50 Thr Asn Glu Tyr Gly Asp Asn Met Gln Ile Ser Gln Asp Asn Val Thr
180 185 190

Glu Leu Phe Ser Ile Ser Asn Ser Leu Ser Leu Ser Phe Pro Asp Gly
195 200 205

55 Val Trp His Met Thr Val Val Cys Val Leu Glu Thr Glu Ser Met Lys
210 215 220

Ile Ser Ser Lys Pro Leu Asn Phe Thr Gln Glu Phe Pro Ser Pro Gln
225 230 235 240

Thr Tyr Trp Lys Glu Ile Thr Ala Ser Val Thr Val Ala Leu Leu Leu
245 250 255

Val Met Leu Leu Ile Ile Val Cys His Lys Lys Pro Asn Gln Pro Ser
260 265 270

Arg Pro Ser Asn Thr Ala Ser Lys Leu Glu Arg Asp Ser Asn Ala Asp
275 280 285

Arg Glu Thr Ile Asn Leu Lys Glu Leu Glu Pro Gln Ile Ala Ser Ala
290 295 300

Lys Pro Asn Ala Glu
305

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1120 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 107..1093

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CACAGGGTGA AAGCTTTGCT TCTCTGCTGC TGTAACAGGG ACTAGCACAG ACACACGGAT 60

GAGTGGGGTC ATTTCCAGAT ATTAGGTCAC AGCAGAAGCA GCCAAA ATG GAT CCC 115
Met Asp Pro
1

CAG TGC ACT ATG GGA CTG AGT AAC ATT CTC TTT GTG ATG GCC TTC CTG 163
Gln Cys Thr Met Gly Leu Ser Asn Ile Leu Phe Val Met Ala Phe Leu
5 10 15

CTC TCT GGT GCT GCT CCT CTG AAG ATT CAA GCT TAT TTC AAT GAG ACT 211
Leu Ser Gly Ala Ala Pro Leu Lys Ile Gln Ala Tyr Phe Asn Glu Thr
20 25 30 35

GCA GAC CTG CCA TGC CAA TTT GCA AAC TCT CAA AAC CAA AGC CTG AGT 259
Ala Asp Leu Pro Cys Gln Phe Ala Asn Ser Gln Asn Gln Ser Leu Ser
40 45 50

GAG CTA GTA GTA TTT TGG CAG GAC CAG GAA AAC TTG GTT CTG AAT GAG 307
Glu Leu Val Val Phe Trp Gln Asp Gln Glu Asn Leu Val Leu Asn Glu
55 60 65

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Sub 35
a1

	GTA TAC TTA GGC AAA GAG AAA TTT GAC AGT GTT CAT TCC AAG TAT ATG Val Tyr Leu Gly Lys Glu Lys Phe Asp Ser Val His Ser Lys Tyr Met	355
	70 75 80	
5	GGC CGC ACA AGT TTT GAT TCG GAC AGT TGG ACC CTG AGA CTT CAC AAT Gly Arg Thr Ser Phe Asp Ser Asp Ser Trp Thr Leu Arg Leu His Asn	403
	85 90 95	
10	CTT CAG ATC AAG GAC AAG GGC TTG TAT CAA TGT ATC ATC CAT CAC AAA Leu Gln Ile Lys Asp Lys Gly Leu Tyr Gln Cys Ile Ile His His Lys	451
	100 105 110 115	
15	AAG CCC ACA GGA ATG ATT CGC ATC CAC CAG ATG AAT TCT GAA CTG TCA Lys Pro Thr Gly Met Ile Arg Ile His Gln Met Asn Ser Glu Leu Ser	499
	120 125 130	
20	GTG CTT GCT AAC TTC AGT CAA CCT GAA ATA GTA CCA ATT TCT AAT ATA Val Leu Ala Asn Phe Ser Gln Pro Glu Ile Val Pro Ile Ser Asn Ile	547
	135 140 145	
25	ACA GAA AAT GTG TAC ATA AAT TTG ACC TGC TCA TCT ATA CAC GGT TAC Thr Glu Asn Val Tyr Ile Asn Leu Thr Cys Ser Ser Ile His Gly Tyr	595
	150 155 160	
30	CCA GAA CCT AAG AAG ATG AGT GTT TTG CTA AGA ACC AAG AAT TCA ACT Pro Glu Pro Lys Lys Met Ser Val Leu Leu Arg Thr Lys Asn Ser Thr	643
	165 170 175	
35	ATC GAG TAT GAT GGT ATT ATG CAG AAA TCT CAA GAT AAT GTC ACA GAA Ile Glu Tyr Asp Gly Ile Met Gln Lys Ser Gln Asp Asn Val Thr Glu	691
	180 185 190 195	
40	CTG TAC GAC GTT TCC ATC AGC TTG TCT GTT TCA TTC CCT GAT GTT ACG Leu Tyr Asp Val Ser Ile Ser Leu Ser Val Ser Phe Pro Asp Val Thr	739
	200 205 210	
45	AGC AAT ATG ACC ATC TTC TGT ATT CTG GAA ACT GAC AAG ACG CGG CTT Ser Asn Met Thr Ile Phe Cys Ile Leu Glu Thr Asp Lys Thr Arg Leu	787
	215 220 225	
50	TTA TCT TCA CCT TTC TCT ATA GAG CTT GAG GAC CCT CAG CCT CCC CCA Leu Ser Ser Pro Phe Ser Ile Glu Leu Glu Asp Pro Gln Pro Pro Pro	835
	230 235 240	
55	GAC CAC ATT CCT TGG ATT ACA GCT GTA CTT CCA ACA GTT ATT ATA TGT Asp His Ile Pro Trp Ile Thr Ala Val Leu Pro Thr Val Ile Ile Cys	883
	245 250 255	
60	GTG ATG GTT TTC TGT CTA ATT CTA TGG AAA TGG AAG AAG AAG AAG CGG Val Met Val Phe Cys Leu Ile Leu Trp Lys Trp Lys Lys Lys Lys Arg	931
	260 265 270 275	
65	CCT CGC AAC TCT TAT AAA TGT GGA ACC AAC ACA ATG GAG AGG GAA GAG Pro Arg Asn Ser Tyr Lys Cys Gly Thr Asn Thr Met Glu Arg Glu Glu	979
	280 285 290	
70	AGT GAA CAG ACC AAG AAA AGA GAA AAA ATC CAT ATA CCT GAA AGA TCT Ser Glu Gln Thr Lys Lys Arg Glu Lys Ile His Ile Pro Glu Arg Ser	1027
	295 300 305	

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Sub
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GAT GAA GCC CAG CGT GTT TTT AAA AGT TCG AAG ACA TCT TCA TGC GAC 1075
 Asp Glu Ala Gln Arg Val Phe Lys Ser Ser Lys Thr Ser Ser Cys Asp
 310 315 320

5 AAA AGT GAT ACA TGT TTT TAATTAAAGA GTAAAGCCCA AAAAAAA 1120
 Lys Ser Asp Thr Cys Phe
 325

10 (2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 329 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Met Asp Pro Gln Cys Thr Met Gly Leu Ser Asn Ile Leu Phe Val Met
 1 5 10 15

25 Ala Phe Leu Leu Ser Gly Ala Ala Pro Leu Lys Ile Gln Ala Tyr Phe
 20 25 30

Asn Glu Thr Ala Asp Leu Pro Cys Gln Phe Ala Asn Ser Gln Asn Gln
 35 40 45

Ser Leu Ser Glu Leu Val Val Phe Trp Gln Asp Gln Glu Asn Leu Val
 50 55 60

Leu Asn Glu Val Tyr Leu Gly Lys Glu Lys Phe Asp Ser Val His Ser
 65 70 75 80

Lys Tyr Met Gly Arg Thr Ser Phe Asp Ser Asp Ser Trp Thr Leu Arg
 85 90 95

40 Leu His Asn Leu Gln Ile Lys Asp Lys Gly Leu Tyr Gln Cys Ile Ile
 100 105 110

His His Lys Lys Pro Thr Gly Met Ile Arg Ile His Gln Met Asn Ser
 115 120 125

45 Glu Leu Ser Val Leu Ala Asn Phe Ser Gln Pro Glu Ile Val Pro Ile
 130 135 140

50 Ser Asn Ile Thr Glu Asn Val Tyr Ile Asn Leu Thr Cys Ser Ser Ile
 145 150 155 160

His Gly Tyr Pro Glu Pro Lys Lys Met Ser Val Leu Leu Arg Thr Lys
 165 170 175

55 Asn Ser Thr Ile Glu Tyr Asp Gly Ile Met Gln Lys Ser Gln Asp Asn
 180 185 190

Val Thr Glu Leu Tyr Asp Val Ser Ile Ser Leu Ser Val Ser Phe Pro
 195 200 205

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 Sub
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Asp Val Thr Ser Asn Met Thr Ile Phe Cys Ile Leu Glu Thr Asp Lys
210 215 220

5 Thr Arg Leu Leu Ser Ser Pro Phe Ser Ile Glu Leu Glu Asp Pro Gln
225 230 235 240

Pro Pro Pro Asp His Ile Pro Trp Ile Thr Ala Val Leu Pro Thr Val
245 250 255

Ile Ile Cys Val Met Val Phe Cys Leu Ile Leu Trp Lys Trp Lys Lys
260 265 270

15 Lys Lys Arg Pro Arg Asn Ser Tyr / Lys Cys Gly Thr Asn Thr Met Glu
 275 280 285

Arg Glu Glu Ser Glu Gln Thr Lys Lys Arg Glu Lys Ile His Ile Pro
290 295 300

20 Glu Arg Ser Asp Glu Ala Gln Arg Val Phe Lys Ser Ser Lys Thr Ser
305 310 315 320

Ser Cys Asp Lys Ser Asp Thr Cys Phe
325

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1161 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 148..1134

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

AGGAGCCTTA GGAGGTACGG GGAGCTCGCA AATACTCCTT TTGGTTTATT CTTACCACCT 60

TGCTTCTGTG TTCCTTGGGA ATGCTGCTGT GCTTATGCAT CTGGTCTCTT TTTGGAGCTA 120

CAGTGGACAG GCATTTGTGA CAGCACT ATG GAT CCC CAG TGC ACT ATG GGA
Met Asp Pro Gln Cys Thr Met Gly

CTG AGT AAC ATT CTC TTT GTG ATG GCC TTC CTG CTC TCT GGT GCT GCT 219
Leu Ser Asn Ile Leu Phe Val Met Ala Phe Leu Leu Ser Gly Ala Ala
10 15 20

CCT CTG AAG ATT CAA GCT TAT TTC AAT GAG ACT GCA GAC CTG CCA TGC 267
Pro Leu Lys Ile Gln Ala Tyr Phe Asn Glu Thr Ala Asp Leu Pro Cys
25 30 35 40

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Sub a1

	CAA	TTT	GCA	AAC	TCT	CAA	AAC	CAA	AGC	CTG	AGT	GAG	CTA	GTA	GTA	TTT	315
	Gln	Phe	Ala	Asn	Ser	Gln	Asn	Gln	Ser	Leu	Ser	Glu	Leu	Val	Val	Phe	
					45					50						55	
5	TGG	CAG	GAC	CAG	GAA	AAC	TTG	GTT	CTG	AAT	GAG	GTA	TAC	TTA	GGC	AAA	363
	Trp	Gln	Asp	Gln	Glu	Asn	Leu	Val	Leu	Asn	Glu	Val	Tyr	Leu	Gly	Lys	
					60					65						70	
10	GAG	AAA	TTT	GAC	AGT	GTT	CAT	TCC	AAG	TAT	ATG	GGC	CGC	ACA	AGT	TTT	411
	Glu	Lys	Phe	Asp	Ser	Val	His	Ser	Lys	Tyr	Met	Gly	Arg	Thr	Ser	Phe	
					75					80						85	
15	GAT	TCG	GAC	AGT	TGG	ACC	CTG	AGA	CTT	CAC	AAT	CTT	CAG	ATC	AAG	GAC	459
	Asp	Ser	Asp	Ser	Trp	Thr	Leu	Arg	Leu	His	Asn	Leu	Gln	Ile	Lys	Asp	
					90					95						100	
20	AAG	GGC	TTG	TAT	CAA	TGT	ATC	ATC	CAT	CAC	AAA	AAG	CCC	ACA	GGA	ATG	507
	Lys	Gly	Leu	Tyr	Gln	Cys	Ile	Ile	His	His	Lys	Lys	Pro	Thr	Gly	Met	
						110										120	
	ATT	CGC	ATC	CAC	CAG	ATG	AAT	TCT	GAA	CTG	TCA	GTG	CTT	GCT	AAC	TTC	555
	Ile	Arg	Ile	His	Gln	Met	Asn	Ser	Glu	Leu	Ser	Val	Leu	Ala	Asn	Phe	
					125					130						135	
25	AGT	CAA	CCT	GAA	ATA	GTA	CCA	ATT	TCT	AAT	ATA	ACA	GAA	AAT	GTG	TAC	603
	Ser	Gln	Pro	Glu	Ile	Val	Pro	Ile	Ser	Asn	Ile	Thr	Glu	Asn	Val	Tyr	
					140					145						150	
30	ATA	AAT	TTG	ACC	TGC	TCA	TCT	ATA	CAC	GGT	TAC	CCA	GAA	CCT	AAG	AAG	651
	Ile	Asn	Leu	Thr	Cys	Ser	Ser	Ile	His	Gly	Tyr	Pro	Glu	Pro	Lys	Lys	
					155					160						165	
35	ATG	AGT	GTT	TTG	CTA	AGA	ACC	AAG	AAT	TCA	ACT	ATC	GAG	TAT	GAT	GGT	699
	Met	Ser	Val	Leu	Leu	Arg	Thr	Lys	Asn	Ser	Thr	Ile	Glu	Tyr	Asp	Gly	
					170					175						180	
40	ATT	ATG	CAG	AAA	TCT	CAA	GAT	AAT	GTC	ACA	GAA	CTG	TAC	GAC	GTT	TCC	747
	Ile	Met	Gln	Lys	Ser	Gln	Asp	Asn	Val	Thr	Glu	Leu	Tyr	Asp	Val	Ser	
						190										200	
	ATC	AGC	TTG	TCT	GTT	TCA	TTC	CCT	GAT	GTT	ACG	AGC	AAT	ATG	ACC	ATC	795
	Ile	Ser	Leu	Ser	Val	Ser	Phe	Pro	Asp	Val	Thr	Ser	Asn	Met	Thr	Ile	
					205					210						215	
45	TTC	TGT	ATT	CTG	GAA	ACT	GAC	AAG	ACG	CGG	CTT	TTA	TCT	TCA	CCT	TTC	843
	Phe	Cys	Ile	Leu	Glu	Thr	Asp	Lys	Thr	Arg	Leu	Leu	Ser	Ser	Pro	Phe	
					220					225						230	
50	TCT	ATA	GAG	CTT	GAG	GAC	CCT	CAG	CCT	CCC	CCA	GAC	CAC	ATT	CCT	TGG	891
	Ser	Ile	Glu	Leu	Glu	Asp	Pro	Gln	Pro	Pro	Pro	Asp	His	Ile	Pro	Trp	
					235					240						245	
55	ATT	ACA	GCT	GTA	CTT	CCA	ACA	GTT	ATT	ATA	TGT	GTG	ATG	GTT	TTC	TGT	939
	Ile	Thr	Ala	Val	Leu	Pro	Thr	Val	Ile	Ile	Cys	Val	Met	Val	Phe	Cys	
					250					255						260	
	CTA	ATT	CTA	TGG	AAA	TGG	AAG	AAG	AAG	AAG	CGG	CCT	CGC	AAC	TCT	TAT	987
	Leu	Ile	Leu	Trp	Lys	Trp	Lys	Lys	Lys	Lys	Arg	Pro	Arg	Asn	Ser	Tyr	
					265					270						275	
																280	

550580-52520280

Sub
at

AAA TGT GGA ACC AAC ACA ATG GAG AGG GAA GAG AGT GAA CAG ACC AAG 1035
Lys Cys Gly Thr Asn Thr Met Glu Arg Glu Glu Ser Glu Gln Thr Lys
285 290 295

5 AAA AGA GAA AAA ATC CAT ATA CCT GAA AGA TCT GAT GAA GCC CAG CGT 1083
Lys Arg Glu Lys Ile His Ile Pro Glu Arg Ser Asp Glu Ala Gln Arg
300 305 310

10 GTT TTT AAA AGT TCG AAG ACA TCT TCA TGC GAC AAA AGT GAT ACA TGT 1131
Val Phe Lys Ser Ser Lys Thr Ser Ser Cys Asp Lys Ser Asp Thr Cys
315 320 325

15 TTT TAATTAAAGA GTAAAGCCCA AAAAAA 1161
Phe

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 629 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..96

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

AGA AGC TGT TTC AGA AGA AAT GAG GCA AGC AGA GAA ACA AAC AAC AGC 48
Arg Ser Cys Phe Arg Arg Asn Glu Ala Ser Arg Glu Thr Asn Asn Ser
1 5 10 15

40 CTT ACC TTC GGG CCT GAA GAA GCA TTA GCT GAA CAG ACC GTC TTC CTT 96
Leu Thr Phe Gly Pro Glu Glu Ala Leu Ala Glu Gln Thr Val Phe Leu
20 25 30

45 TAGTTCTTCT CTGTCCATGT GGGATACATG GTATTATGTG GCTCATGAGG TACAATCTTT 156

CTTTCAGCAC CGTGCTAGCT GATCTTTCGG ACAACTTGAC ACAAGATAGA GTTAAGTGGG 216

50 AAGAGAAAGC CTTGAATGAG GATTTCTTTC CATCAGGAAG CTACGGGCAA GTTTGCTGGG 276

CCTTTGATTG CTTGATGACT GAAGTGGAAG GGCTGAGCCC ACTGTGGGTG GTGCTAGAAA 336

TGGGCAGGGG CAGGTGACCC TGGGTGGTAT AAGAAAAAGA GCTGTCACTA AAAGGAGAGG 396

55 TGCCTAGTCT TACTGCAACT TGATATGTCA TGTTTGTTG GTGTCTGTGG GAGGCCTGCC 456

CTTTTCTGAA GAGAAGTGGT GGGAGAGTGG ATGGGGTGGG GGCAGAGGAA AAGTGGGGGA 516

GAGGGCCTGG GAGGAGAGGA GGGAGGGGGA CGGGGTGGGG GTGGGGAAAA CTATGGTTGG 576

96025525-083095

Sub
B5
Cal

GATGTAAAA CGGATAATAA TATAAATATT AAATAAAAAG AGAGTATTGA GCA

629

5 (2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Arg Ser Cys Phe Arg Arg Asn Glu Ala Ser Arg Glu Thr Asn Asn Ser
 1 5 10 15

Leu Thr Phe Gly Pro Glu Glu Ala Leu Ala Glu Gln Thr Val Phe Leu
 20 25 30

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 379 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..69

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TGC TTT GCC CCA AGA TGC AGA GAG AGA AGG AGG AAT GAG AGA TTG AGA
 Cys Phe Ala Pro Arg Cys Arg Glu Arg Arg Arg Asn Glu Arg Leu Arg
 1 5 10 15 48

AGG GAA AGT GTA CGC CCT GTA TAACAGTGTG CGCAGAAGCA AGGGGCTGAA
 Arg Glu Ser Val Arg Pro Val
 20 99

AAGATCTGAA GGTAGCCTCC GTCATCTCTT CTGGGATACA TGGATCGTGG GGATCATGAG
 159

GCATTCTTCC CTTAACAAAT TTAAGCTGTT TTACCCACTA CCTCACCTTC TTAAAAACCT
 219

CTTTCAGATT AAGCTGAACA GTTACAAGAT GGCTGGCATC CCTCTCCTTT CTCCCCATAT
 279

GCAATTTGCT TAATGTAACC TCTTCTTTTG CCATGTTTCC ATTCTGCCAT CTTGAATTGT
 339

CTTGTCAGCC AATTCATTAT CTATTAAACA CTAATTTGAG
 379

08702525-083096

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Cys Phe Ala Pro Arg Cys Arg Glu Arg Arg Arg Asn Glu Arg Leu Arg
 1 5 10 15
 Arg Glu Ser Val Arg Pro Val
 20

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 1..135

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CAC AAG AAG CCG AAT CAG CCT AGC AGG CCC AGC AAC ACA GCC TCT AAG 48
 His Lys Lys Pro Asn Gln Pro Ser Arg Pro Ser Asn Thr Ala Ser Lys
 1 5 10 15
 TTA GAG CGG GAT AGT AAC GCT GAC AGA GAG ACT ATC AAC CTG AAG GAA 96
 Leu Glu Arg Asp Ser Asn Ala Asp Arg Glu Thr Ile Asn Leu Lys Glu
 20 25 30
 CTT GAA CCC CAA ATT GCT TCA GCA AAA CCA AAT GCA GAG TGAAGGCAGT 145
 Leu Glu Pro Gln Ile Ala Ser Ala Lys Pro Asn Ala Glu
 35 40 45
 GAGAGCCTGA GGAAAGAGTT AAAAATTGCT TTGCCTGAAA TAAGAAGTGC AGAGTTTCTC 205
 AGAATTCAAA AATGTTCTCA GCTGATTGGA ATTCTACAGT TGAATAATTA AAGAAC 261

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

03702525-033096

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

5 His Lys Lys Pro Asn Gln Pro Ser Arg Pro Ser Asn Thr Ala Ser Lys
1 5 10 15
Leu Glu Arg Asp Ser Asn Ala Asp Arg Glu Thr Ile Asn Leu Lys Glu
20 25 30
10 Leu Glu Pro Gln Ile Ala Ser Ala Lys Pro Asn Ala Glu
35 40 45

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 1..183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

AAA TGG AAG AAG AAG AAG CGG CCT CGC AAC TCT TAT AAA TGT GGA ACC 48
Lys Trp Lys Lys Lys Lys Arg Pro Arg Asn Ser Tyr Lys Cys Gly Thr
1 5 10 15
35 AAC ACA ATG GAG AGG GAA GAG AGT GAA CAG ACC AAG AAA AGA GAA AAA 96
Asn Thr Met Glu Arg Glu Glu Ser Glu Gln Thr Lys Lys Arg Glu Lys
20 25 30
40 ATC CAT ATA CCT GAA AGA TCT GAT GAA GCC CAG CGT GTT TTT AAA AGT 144
Ile His Ile Pro Glu Arg Ser Asp Glu Ala Gln Arg Val Phe Lys Ser
35 40 45
45 TCG AAG ACA TCT TCA TGC GAC AAA AGT GAT ACA TGT TTT TAATTAAAGA 193
Ser Lys Thr Ser Ser Cys Asp Lys Ser Asp Thr Cys Phe
50 55 60
GTAAAGCCCA AAAAAA 210

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

08702525-083029

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

5 Lys Trp Lys Lys Lys Lys Arg Pro Arg Asn Ser Tyr Lys Cys Gly Thr
 1 5 10 15
 Asn Thr Met Glu Arg Glu Glu Ser Glu Gln Thr Lys Lys Arg Glu Lys
 20 25 30
 10 Ile His Ile Pro Glu Arg Ser Asp Glu Ala Gln Arg Val Phe Lys Ser
 35 40 45
 Ser Lys Thr Ser Ser Cys Asp Lys Ser Asp Thr Cys Phe
 50 55 60

15 (2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 359 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 249..359

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GAGTTTTATA CCTCAATAGA CTCTTACTAG TTTCTCTTTT TCAGGTTGTG AAACCTCAACC 60
 35 TTCAAAGACA CTCTGTTCCA TTTCTGTGGA CTAATAGGAT CATCTTTAGC ATCTGCCGGG 120
 TGGATGCCAT CCAGGCTTCT TTTTCTACAT CTCTGTTTCT CGATTTTTGT GAGCCTAGGA 180
 40 GGTGCCTAAG CTCCATTGGC TCTAGATTCC TGGCTTTCCC CATCATGTTC TCAAAGCAT 240
 CTGAAGCT ATG GCT TGC AAT TGT CAG TTG ATG CAG GAT ACA CCA CTC CTC 290
 Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu
 1 5 10
 45 AAG TTT CCA TGT CCA AGG CTC AAT CTT CTC TTT GTG CTG CTG ATT CGT 338
 Lys Phe Pro Cys Pro Arg Leu Asn Leu Leu Phe Val Leu Leu Ile Arg
 15 20 25 30
 50 CTT TCA CAA GTG TCT TCA GAT 359
 Leu Ser Gln Val Ser Ser Asp
 35

55 (2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

03702525-033096

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu Lys Phe
 1 5 10 15
 Pro Cys Pro Arg Leu Ile Leu Leu Phe Val Leu Leu Ile Arg Leu Ser
 20 25 30
 Gln Val Ser Ser Asp
 35

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 416 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 318..416

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

CCAAAGAAAA AGTGATTTGT CATTGCTTTA TAGACTGTAA GAAGAGAACA TCTCAGAAGT 60
 GGAGTCTTAC CCTGAAATCA AAGGATTTAA AGAAAAAGTG GAATTTTTCT TCAGCAAGCT 120
 GTGAAACTAA ATCCACAACC TTTGGAGACC CAGGAACACC CTCCAATCTC TGTGTGTTTT 180
 GTAAACATCA CTGGAGGGTC TTCTACGTGA GCAATTGGAT TGTCATCAGC CCTGCCTGTT 240
 TTGCACCTGG GAAGTGCCCT GGTCTTACTT GGGTCCAAAT TGTGCTTTT CACTTTTGAC 300
 CCTAAGCATC TGAAGCC ATG GGC CAC ACA CGG AGG CAG GGA ACA TCA CCA 350
 Met Gly His Thr Arg Arg Gln Gly Thr Ser Pro
 1 5 10
 TCC AAG TGT CCA TAC CTG AAT TTC TTT CAG CTC TTG GTG CTG GCT GGT 398
 Ser Lys Cys Pro Tyr Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly
 15 20 25
 CTT TCT CAC TTC TGT TCA 416
 Leu Ser His Phe Cys Ser
 30

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids

960E80 52520/80

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Met Gly His Thr Arg Arg Gln Gly Thr Ser Pro Ser Lys Cys Pro Tyr
1 5 10 15
Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly Leu Ser His Phe Cys
20 25 30

Ser

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 99..113

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GGAGCAAGCA GACGCGTAAG AGTGGCTCCT GTAGGCAGCA CGGACTTGAA CAACCAGACT 60
CCTGTAGACG TGTTCCAGAA CTTACGGAAG CACCCACG ATG GAC CCC AGA TGC 113
Met Asp Pro Arg Cys
1 5

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Met Asp Pro Arg Cys
1 5

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 124 base pairs

03702525-033096

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 107..124

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

15 CACAGGGTGA AAGCTTTGCT TCTCTGCTGC TGTAACAGGG ACTAGCACAG ACACACGGAT 60

GAGTGGGGTC ATTTCCAGAT ATTAGGTCAC AGCAGAAGCA GCCAAA ATG GAT CCC 115
Met Asp Pro

20 CAG TGC ACT 1
Gln Cys Thr 124
5

25 (2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Met Asp Pro Gln Cys Thr
1 5

40 (2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

50 (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 148..195

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

AGGAGCCTTA GGAGGTACGG GGAGCTCGCA AATACTCCTT TTGGTTTATT CTTACCACCT

60

00702525-003096

TGCTTCTGTG TTCCTTGGGA ATGCTGCTGT GCTTATGCAT CTGGTCTCTT TTTGGAGCTA 120

CAGTGGACAG GCATTTGTGA CAGCACT ATG GGA CTG AGT AAC ATT CTC TTT 171
Met Gly Leu Ser Asn Ile Leu Phe
1 5

GTG ATG GCC TTC CTG CTC TCT GGT 195
Val Met Ala Phe Leu Leu Ser Gly
10 15

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Met Gly Leu Ser Asn Ile Leu Phe Val Met Ala Phe Leu Leu Ser Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

CCAACATAAC TGAGTCTGGA AA 22

(2) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

CTGGATTCTG ACTCACCTTC A 21

(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs

08702525-083095

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

AGGTTAAGAG TGGTAGAGCC A

21

10

(2) INFORMATION FOR SEQ ID NO: 46:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

AATACCATGT ATCCCACATG G

21

25

(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

CTGAAGCTAT GGCTTGCAAT T

21

40

(2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:

45

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

TGGCTTCTCT TTCCTTACCT T

21

(2) INFORMATION FOR SEQ ID NO: 49:

55

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

GCAAATGGTA GATGAGACTG T

(2) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

CAACCGAGAA ATCTACCACT AA

(2) INFORMATION FOR SEQ ID NO: 51:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

GCCGGTAACA AGTCTCTTCA

(2) INFORMATION FOR SEQ ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

AAAAGCTCTA TAGCATTCTG TC

(2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

ACTGACTTGG ACAGTTGTTC A

21

5 (2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

TTTGATGGAC AACTTTACTA

20

20 (2) INFORMATION FOR SEQ ID NO: 55:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

CAGCTCACTC AGGCTTATGT

20

(2) INFORMATION FOR SEQ ID NO: 56:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

45 AAACAGCATC TGAGATCAGC A

21

(2) INFORMATION FOR SEQ ID NO: 57:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

CTGAGATCAG CAAGACTGTC

20

960E80-52520/80

Sub
a1

(2) INFORMATION FOR SEQ ID NO: 58:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

CTGAAGCTAT GGCTTGCAAT T

21

(2) INFORMATION FOR SEQ ID NO: 59:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

ACAAGTGTCT TCAGATGTTG AT

22

(2) INFORMATION FOR SEQ ID NO: 60:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

CTGGATTCTG ACTCACCTTC A

21

(2) INFORMATION FOR SEQ ID NO: 61:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

CCAGGTGAAG TCCTCTGACA

20

(2) INFORMATION FOR SEQ ID NO: 62:

08702525-083006

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351

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1417 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 249..884

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

GAGTTTTATA CCTCAATAGA CTCTACTAG TTTCTCTTTT TCAGGTTGTG AAACCTCAACC 60
 TTCAAAGACA CTCTGTTCCA TTTCTGTGGA CTAATAGGAT CATCTTTAGC ATCTGCCGGG 120
 TGGATGCCAT CCAGGCTTCT TTTTCTACAT CTCTGTTTCT CGATTTTGTG GAGCCTAGGA 180
 GGTGCCTAAG CTCCATTGGC TCTAGATTCC TGGCTTTCCC CATCATGTTT TCCAAAGCAT 240
 CTGAAGCT ATG GCT TGC AAT TGT CAG TTG ATG CAG GAT ACA CCA CTC CTC 290
 Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu
 1 5 10
 AAG TTT CCA TGT CCA AGG CTC AAT CTT CTC TTT GTG CTG CTG ATT CGT 338
 Lys Phe Pro Cys Pro Arg Leu Asn Leu Leu Phe Val Leu Leu Ile Arg
 15 20 25 30
 CTT TCA CAA GTG TCT TCA GAT GTT GAT GAA CAA CTG TCC AAG TCA GTG 386
 Leu Ser Gln Val Ser Ser Asp Val Asp Glu Gln Leu Ser Lys Ser Val
 35 35 40 45
 AAA GAT AAG GTA TTG CTG CCT TGC CGT TAC AAC TCT CCT CAT GAA GAT 434
 Lys Asp Lys Val Leu Leu Pro Cys Arg Tyr Asn Ser Pro His Glu Asp
 40 50 55 60
 GAG TCT GAA GAC CGA ATC TAC TGG CAA AAA CAT GAC AAA GTG GTG CTG 482
 Glu Ser Glu Asp Arg Ile Tyr Trp Gln Lys His Asp Lys Val Val Leu
 65 70 75
 TCT GTC ATT GCT GGG AAA CTA AAA GTG TGG CCC GAG TAT AAG AAC CGG 530
 Ser Val Ile Ala Gly Lys Leu Lys Val Trp Pro Glu Tyr Lys Asn Arg
 80 85 90
 ACT TTA TAT GAC AAC ACT ACC TAC TCT CTT ATC ATC CTG GGC CTG GTC 578
 Thr Leu Tyr Asp Asn Thr Thr Tyr Ser Leu Ile Ile Leu Gly Leu Val
 95 100 105 110
 CTT TCA GAC CGG GGC ACA TAC AGC TGT GTC GTT CAA AAG AAG GAA AGA 626
 Leu Ser Asp Arg Gly Thr Tyr Ser Cys Val Val Gln Lys Lys Glu Arg
 115 120 125
 GGA ACG TAT GAA GTT AAA CAC TTG GCT TTA GTA AAG TTG TCC ATC AAA 674
 Gly Thr Tyr Glu Val Lys His Leu Ala Leu Val Lys Leu Ser Ile Lys
 130 135 140

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5 CCC CCA GAA GAC CCT CCT GAT AGC AAG AAC ACA CTT GTG CTC TTT GGG 722
Pro Pro Glu Asp Pro Pro Asp Ser Lys Asn Thr Leu Val Leu Phe Gly
145 150 155

10 GCA GGA TTC GGC GCA GTA ATA ACA GTC GTC GTC ATC GTT GTC ATC ATC 770
Ala Gly Phe Gly Ala Val Ile Thr Val Val Val Ile Val Val Ile Ile
160 165 170

15 AAA TGC TTC TGT AAG CAC AGA AGC TGT TTC AGA AGA AAT GAG GCA AGC 818
Lys Cys Phe Cys Lys His Arg Ser Cys Phe Arg Arg Asn Glu Ala Ser
175 180 185 190

20 AGA GAA ACA AAC AAC AGC CTT ACC TTC GGG CCT GAA GAA GCA TTA GCT 866
Arg Glu Thr Asn Asn Ser Leu Thr Phe Gly Pro Glu Glu Ala Leu Ala
195 200 205

25 GAA CAG ACC GTC TTC CTT TAGTTCTTCT CTGTCCATGT GGGATACATG GTATTATGTG 924
Glu Gln Thr Val Phe Leu
210

30 GCTCATGAGG TACAATCTTT CTTTCAGCAC CGTGCTAGCT GATCTTTCGG ACAACTTGAC 984

35 ACAAGATAGA GTTAACTGGG AAGAGAAAGC CTTGAATGAG GATTTCTTTC CATCAGGAAG 1044

40 CTACGGGCAA GTTTGCTGGG CCTTTGATTG CTTGATGACT GAAGTGGAAA GGCTGAGCCC 1104

45 ACTGTGGGTG GTGCTAGCCC TGGGCAGGGG CAGGTGACCC TGGGTGGTAT AAGAAAAAGA 1164

50 GCTGTCACTA AAAGGAGAGG TGCCTAGTCT TACTGCAACT TGATATGTCA TGTTTGTTG 1224

55 GTGTCTGTGG GAGGCCTGCC CTTTCTGAA GAGAAGTGGT GGCAGAGTGG ATGGGGTGGG 1284

60 GGCAGAGGAA AAGTGGGGGA GAGGCCTGG GAGGAGAGGA GGGAGGGGGA CGGGGTGGGG 1344

65 GTGGGGAAAA CTATGGTTGG GATGTAAAAA CGGATAATAA TATAAATATT AAATAAAAAG 1404

70 AGAGTATTGA GCA 1417

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu Lys Phe
1 5 10 15

Pro Cys Pro Arg Leu Ile Leu Leu Phe Val Leu Leu Ile Arg Leu Ser
20 25 30

Gln Val Ser Ser Asp Val Asp Glu Gln Leu Ser Lys Ser Val Lys Asp
35 40 45

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 960330-0330096

Lys Val Leu Leu Pro Cys Arg Tyr Asn Ser Pro His Glu Asp Glu Ser
50 55 60

5 Glu Asp Arg Ile Tyr Trp Gln Lys His Asp Lys Val Val Leu Ser Val
65 70 75 80

Ile Ala Gly Lys Leu Lys Val Trp Pro Glu Tyr Lys Asn Arg Thr Leu
85 90 95

10 Tyr Asp Asn Thr Thr Tyr Ser Leu Ile Ile Leu Gly Leu Val Leu Ser
100 105 110

15 Asp Arg Gly Thr Tyr Ser Cys Val Val Gln Lys Lys Glu Arg Gly Thr
115 120 125

Tyr Glu Val Lys His Leu Ala Leu Val Lys Leu Ser Ile Lys Pro Pro
130 135 140

20 Glu Asp Pro Pro Asp Ser Lys Asn Thr Leu Val Leu Phe Gly Ala Gly
145 150 155 160

Phe Gly Ala Val Ile Thr Val Val Val Ile Val Val Ile Ile Lys Cys
165 170 175

25 Phe Cys Lys His Arg Ser Cys Phe Arg Arg Asn Glu Ala Ser Arg Glu
180 185 190

30 Thr Asn Asn Ser Leu Thr Phe Gly Pro Glu Glu Ala Leu Ala Glu Gln
195 200 205

Thr Val Phe Leu
210

35

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 1606 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

45

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 249..926

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GAGTTTATA CCTCAATAGA CTCTTACTAG TTTCTCTTTT TCAGGTTGTG AAACCTCAACC 60
55 TTCAAAGACA CTCTGTTCCA TTTCTGTGGA CTAATAGGAT CATCTTTAGC ATCTGCCGGG 120
TGGATGCCAT CCAGGCTTCT TTTTCTACAT CTCTGTTTCT CGATTTTGT GAGCCTAGGA 180
GGTGCCTAAG CTCCATTGGC TCTAGATTCC TGGCTTTCCC CATCATGTTC TCCAAAGCAT 240

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	CTGAAGCT	ATG	GCT	TGC	AAT	TGT	CAG	TTG	ATG	CAG	GAT	ACA	CCA	CTC	CTC	290	
	Met	Ala	Cys	Asn	Cys	Gln	Leu	Met	Gln	Asp	Thr	Pro	Leu	Leu			
	1					5						10					
5	AAG	TTT	CCA	TGT	CCA	AGG	CTC	AAT	CTT	CTC	TTT	GTG	CTG	CTG	ATT	CGT	338
	Lys	Phe	Pro	Cys	Pro	Arg	Leu	Asn	Leu	Leu	Phe	Val	Leu	Leu	Ile	Arg	
	15					20					25					30	
10	CTT	TCA	CAA	GTG	TCT	TCA	GAT	GTT	GAT	GAA	CAA	CTG	TCC	AAG	TCA	GTG	386
	Leu	Ser	Gln	Val	Ser	Ser	Asp	Val	Asp	Glu	Gln	Leu	Ser	Lys	Ser	Val	
					35					40					45		
15	AAA	GAT	AAG	GTA	TTG	CTG	CCT	TGC	CGT	TAC	AAC	TCT	CCT	CAT	GAA	GAT	434
	Lys	Asp	Lys	Val	Leu	Leu	Pro	Cys	Arg	Tyr	Asn	Ser	Pro	His	Glu	Asp	
				50					55					60			
20	GAG	TCT	GAA	GAC	CGA	ATC	TAC	TGG	CAA	AAA	CAT	GAC	AAA	GTG	GTG	CTG	482
	Glu	Ser	Glu	Asp	Arg	Ile	Tyr	Trp	Gln	Lys	His	Asp	Lys	Val	Val	Leu	
			65					70					75				
25	TCT	GTC	ATT	GCT	GGG	AAA	CTA	AAA	GTG	TGG	CCC	GAG	TAT	AAG	AAC	CGG	530
	Ser	Val	Ile	Ala	Gly	Lys	Leu	Lys	Val	Trp	Pro	Glu	Tyr	Lys	Asn	Arg	
	80						85					90					
30	ACT	TTA	TAT	GAC	AAC	ACT	ACC	TAC	TCT	CTT	ATC	ATC	CTG	GGC	CTG	GTC	578
	Thr	Leu	Tyr	Asp	Asn	Thr	Thr	Tyr	Ser	Leu	Ile	Ile	Leu	Gly	Leu	Val	
	95					100					105					110	
35	CTT	TCA	GAC	CGG	GGC	ACA	TAC	AGC	TGT	GTC	GTT	CAA	AAG	AAG	GAA	AGA	626
	Leu	Ser	Asp	Arg	Gly	Thr	Tyr	Ser	Cys	Val	Val	Gln	Lys	Lys	Glu	Arg	
					115					120					125		
40	GGA	ACG	TAT	GAA	GTT	AAA	CAC	TTG	GCT	TTA	GTA	AAG	TTG	TCC	ATC	AAA	674
	Gly	Thr	Tyr	Glu	Val	Lys	His	Leu	Ala	Leu	Val	Lys	Leu	Ser	Ile	Lys	
				130				135						140			
45	CCC	CCA	GAA	GAC	CCT	CCT	GAT	AGC	AAG	AAC	ACA	CTT	GTG	CTC	TTT	GGG	722
	Pro	Pro	Glu	Asp	Pro	Pro	Asp	Ser	Lys	Asn	Thr	Leu	Val	Leu	Phe	Gly	
			145					150					155				
50	GCA	GGA	TTC	GGC	GCA	GTA	ATA	ACA	GTC	GTC	GTC	ATC	GTT	GTC	ATC	ATC	770
	Ala	Gly	Phe	Gly	Ala	Val	Ile	Thr	Val	Val	Val	Ile	Val	Val	Ile	Ile	

AAT GAA CCA CAG TAGTTCTGCT GTTCTGAGG ACGTAGTTTA GAGACTGAAT
 Asn Glu Pro Gln
 225

966

5 TCTTTGGAAA GGACATAGGG ACAGTTTGCA CATTGCTTG CACATCACAC ACACACACAC 1026
 ACACACACAC ACACACACAC ACACACACAC ACACACACAC ACACACACAC TCTCTCTCTC 1086
 10 TCTCTCTCTC GATACCTTAG GATAGGGTTC TACCCTGTTG CTCAGTGACA AAGAATCACT 1146
 CTGTGGCGGA GGCAGGCTTC AAGCTTGACG CAATCCTCCT GCACCAGTTT CCTGAGTGCC 1206
 AGACTTCCAG GTGTAAGCTA TGGCACTTAG CAGAACACTA GCTGAATCAA TGAAGACACT 1266
 15 GAGGTTCCAA GAGGGAACCT GAATTATGAA GGTGAGTCAG AATCCAGATT TCCTGGCTCT 1326
 ACCACTCTTA ACCTGTATCT GTTAGACCCC AAGCTCTGAG CTCATAGACA AGCTAATTTA 1386
 20 AAATGCTTTT TAATAAGCAG AAGGCTCAGT TAGTACGGGG TTCAGGATAC TGCTTACTGG 1446
 CAATATTTGA CTAGCCTCTA TTTTGTGTTGT TTTTAAAGG CCTACTGACT GTAGTGTAAT 1506
 TTGTAGGAAA CATGTTGCTA TGTATACCCA TTTGAGGGTA ATAAAAATGT TGGTAATTTT 1566
 25 CAGCCAGCAC TTTCCAGGTA TTTCCCTTTT TATCCTTCAT 1606

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 226 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

40 Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu Lys Phe
 1 5 10 15
 Pro Cys Pro Arg Leu Ile Leu Leu Phe Val Leu Leu Ile Arg Leu Ser
 20 25 30
 45 Gln Val Ser Ser Asp Val Asp Glu Gln Leu Ser Lys Ser Val Lys Asp
 35 40 45
 Lys Val Leu Leu Pro Cys Arg Tyr Asn Ser Pro His Glu Asp Glu Ser
 50 55 60
 Glu Asp Arg Ile Tyr Trp Gln Lys His Asp Lys Val Val Leu Ser Val
 65 70 75 80
 55 Ile Ala Gly Lys Leu Lys Val Trp Pro Glu Tyr Lys Asn Arg Thr Leu
 85 90 95
 Tyr Asp Asn Thr Thr Tyr Ser Leu Ile Ile Leu Gly Leu Val Leu Ser
 100 105 110

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 96080-5220/80

- 96 -

Asp Arg Gly Thr Tyr Ser Cys Val Val Gln Lys Lys Glu Arg Gly Thr
115 120 125

5 Tyr Glu Val Lys His Leu Ala Leu Val Lys Leu Ser Ile Lys Pro Pro
130 135 140

Glu Asp Pro Pro Asp Ser Lys Asn Thr Leu Val Leu Phe Gly Ala Gly
145 150 155 160

10 Phe Gly Ala Val Ile Thr Val Val Val Ile Val Val Ile Ile Lys Cys
165 170 175

Phe Cys Lys His Gly Leu Ile Tyr His Leu Gln Leu Thr Ser Ser Ala
180 185 190

Lys Asp Phe Arg Asn Leu Ala Leu Pro Trp Leu Cys Lys His Gly Ser
195 200 205

20 Leu Gly Glu Ala Ser Ala Val Ile Cys Arg Ser Thr Gln Thr Asn Glu
210 215 220

Pro Gln
225

Sub
al 15
concl

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960280 52520480